

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:18 ; Search time 40 Seconds
(without alignments)
401.705 Million cell updates/sec

Title: US-10-617-955-2-COPY
Perfect score: 860
Sequence: 1 YSTEVEAAVNRLVNLVLRAS.....VSKAGLGELYFERLTUKHD 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	839	97.6	175	1 FRHOL	ferritin light cha
2	756	87.9	175	1 FRHOL	ferritin light cha
3	745	86.6	175	2 JC7238	ferritin protein 1
4	738	85.8	175	2 S01239	ferritin light cha
5	726	84.4	183	1 FRRTL	ferritin light cha
6	724	84.2	183	2 I54774	ferritin light cha
7	712	82.8	183	2 B33355	ferritin light cha
8	536	62.3	176	1 FRFGL	ferritin, tadpole
9	535	62.2	176	2 A27805	ferritin chain H -
10	518	60.2	176	1 FRXL	ferritin heavy cha
11	513	59.7	176	2 C27805	ferritin chain M -
12	495	57.6	180	2 A26886	ferritin heavy cha
13	493	57.3	181	2 A39884	ferritin heavy cha
14	490	57.0	182	2 S06070	ferritin heavy cha
15	487	56.6	183	1 FRHUL	ferritin heavy cha
16	481	55.9	164	2 I46710	ferritin heavy cha
17	463.5	53.9	174	2 S45603	ferritin, soma - g
18	457.5	53.2	174	2 B27805	ferritin chain L -
19	422.5	49.1	170	2 T33854	hypothetical prote
20	389.5	45.3	170	2 T31870	hypothetical prote
21	387.5	45.1	172	2 A45628	ferritin heavy cha
22	382	44.4	181	2 S62651	ferritin - signal
23	375.5	43.7	173	1 B45628	ferritin heavy cha
24	368	42.8	141	2 I48109	ferritin heavy cha
25	336	39.1	78	2 S06906	ferritin light cha
26	334.5	38.9	250	2 A40992	ferritin precursor
27	334.5	38.9	254	2 T08593	ferritin precursor
28	334.5	38.9	259	2 T47726	hypothetical prote
29	332	38.6	254	1 FRFBH	ferritin heavy cha

30	332	38.6	256	2 T08123	ferritin 3 precurs
31	329.5	38.3	259	2 G84827	probable ferritin
32	324.5	37.7	250	2 T08124	ferritin 2 precurs
33	315.5	36.7	255	2 S71880	ferritin 1 precurs
34	315.5	36.7	285	2 S22498	ferritin 1 precurs
35	308	35.8	300	2 S24057	ferritin 2 precurs
36	295.5	34.4	253	2 S27358	ferritin precursor
37	242	28.1	85	2 S68315	ferritin H chain -
38	238	27.7	80	2 S06905	ferritin heavy cha
39	213	24.8	71	2 S06279	ferritin heavy cha
40	209	24.3	49	2 S68314	ferritin L chain -
41	196.5	22.8	239	2 S45604	ferritin precursor
42	175	20.3	43	2 S04979	ferritin light cha
43	169.5	19.7	164	2 E72293	ferritin - Thermot
44	148	17.2	171	2 G69077	ferritin like prot
45	142.5	16.6	229	2 S13978	artemin - brine sh

ALIGNMENTS

RESULT 1

FRHOL

ferritin light chain - horse

C:Species: Equus caballus (domestic horse)

C>Date: 01-Sep-1981 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: S36118; A03267

R:Takeda, S.; Ohta, M.; Ebina, S.; Nagayama, K.

Biochim. Biophys. Acta 1174, 218-220, 1993

A>Title: Cloning, expression and characterization of horse L-ferritin in Escherichia coli

A:Reference number: S36118; MUID:93363645; PMID:8357841

A:Accession: S36118

A:Molecule type: mRNA

A:Residues: 1-175 <TAK>

A:Cross-references: UNIPROT:P02791; GB:D14523; NID:G406208; PIDN:BA03396.1; PID:G406209

A:Experimental source: liver

R:Heusterspreute, M.; Crichton, R.R.

FEBS Lett. 129, 322-327, 1981

A>Title: Amino acid sequence of horse spleen apoferritin.

A:Reference number: A91294; MUID:82027739; PMID:7026284

A:Accession: A03267

A:Molecule type: protein

A:Residues: 2-93, 'L', 95-175 <HEU>

A:Experimental source: spleen

R:Peteg, G.A.; Stansfield, R.F.D.; Bourne, P.E.; Harrison, P.M.

Nature 288, 298-300, 1980

A>Title: Helix packing and subunit conformation in horse spleen apoferritin.

A:Reference number: A93239; MUID:81052459; PMID:7432529

A:Contents: annotation; X-ray crystallography, 2.8 angstroms

C:Comment: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic

chains a central cavity in which the polymeric ferric iron core is deposited.

C:Comment: There are two types of ferritin subunits: L (light) chain and H (heavy) chain.

C:Superfamily: ferritin

C:Keywords: acetylated amino end; iron; iron storage; liver; metalloprotein; multimer; s

F/2-175/Product: ferritin light chain #status experimental <MAT>

F/2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F/54,57,58,61,64/Binding site: iron (Glu) #status predicted

Query Match 97.6%; Score 839; DB 1; Length 175;

Best Local Similarity 97.6%; Pred. No. 7.1e-64;

Matches 163; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY	1	YSTEVEAAVNRLVNLVLRASYTYLSIGFYFDRDDVALBGCYHFFRELAEEKREGARLLK	60
DB	9	YSTEVEAAVNRLVNLVLRASYTYLSIGFYFDRDDVALBGCYHFFRELAEEKREGARLLK	68
QY	61	MONRGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKADPHLCD	120
DB	69	MONRGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSAQADPHLCD	128
QY	121	FLSHFLDEEVKLIRKMGHILTNIQRLYKAGLGELYFERLTUKHD	167

Db 129 FLESHFLDEEVKLIKMGDHLTNIQRLVGSQAGIGEYLFERLTLKHD 175

RESULT 2

ferritin light chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jun-1983 #sequence revision 03-May-1996 #text_change 09-Jul-2004
C/Accession: B23920; B24844; A94043; A91317; A91308; I37137; S68943; A03266
R/Boyd, D.; Vecoli, C.; Belcher, D.M.; Jain, S.K.; Drysdale, J.W.
J. Biol. Chem. 260, 11755-11761, 1985
A/Title: Structural and functional relationships of human ferritin H and L chains deduced
A/Reference number: A92494; MUID:86008223; PMID:3840162
A/Accession: B23920
A/Molecule type: mRNA
A/Residues: 1-175 <BOY>
A/Cross-references: UNIPROT:P02792; GB:M1147; NID:g182513; PIDN:AAA52439.1; PID:g182514
R/Chou, C.C.; Gatti, R.A.; Fuller, M.L.; Concannon, P.; Wong, A.; Chada, S.; Davis, R.C.
Mol. Cell. Biol. 6, 566-573, 1986
A/Title: Structure and expression of ferritin genes in a human promyelocytic cell line C
A/Reference number: A93087; MUID:87064341; PMID:3023856
A/Accession: B24844
A/Molecule type: mRNA
A/Residues: 33-175 <CHO>
A/Cross-references: GB:M12938; NID:g182515; PIDN:AAA52440.1; PID:g182516
R/Dorner, M.H.; Saifeld, J.; Will, H.; Leibold, E.A.; Vass, J.K.; Munro, H.N.
Proc. Natl. Acad. Sci. U.S.A. 82, 3139-3143, 1985
A/Title: Structure of human ferritin light subunit messenger RNA: comparison with heavy
A/Reference number: A94043; MUID:85216457; PMID:3858810
A/Accession: A94043
A/Molecule type: mRNA
A/Residues: 1-101, 'T', 103-175 <DOR>
A/Cross-references: GB:M10119; NID:g182517; PIDN:AAA35831.1; PID:g182518
A/Experimental source: monocyte-like leukemia cell line U937
R/Addison, J.M.; Fitton, J.E.; Lewis, W.G.; May, K.; Harrison, P.M.
FEBS Lett. 164, 139-144, 1983
A/Title: The amino acid sequence of human liver apoferritin.
A/Reference number: A91317; MUID:84085077; PMID:6653779
A/Accession: A91317
A/Molecule type: protein
A/Residues: 2-36/41-53, 'Q', 55-86, 'Q', 88-174, 'ND' <ADD>
A/Experimental source: liver
A/Note: some peptides were positioned by homology
R/Wuetefeld, C.; Crichton, R.R.
FEBS Lett. 150, 43-48, 1982
A/Title: The amino acid sequence of human spleen apoferritin.
A/Reference number: A91308
A/Accession: A91308
A/Molecule type: protein
A/Residues: 2-18, 'Y', 20-25, 'Y', 27-39, 'BY', 42-152, 'RK', 155-175 <WUS>
A/Experimental source: spleen
A/Note: the order of residues 2-7, 40-41, and 153-154 was not determined. Some peptides
R/Santorio, C.; Marone, M.; Ferrone, M.; Costanzo, F.; Colombo, M.; Minganti, C.; Cortese
Nucleic Acids Res. 14, 2863-2876, 1986
A/Title: Cloning of the gene coding for human L apoferritin.
A/Reference number: I37137; MUID:86176772; PMID:3754330
A/Accession: I37137
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-83 <RES>
A/Cross-references: EMBL:X03742; NID:g28518; PIDN:CAA27382.1; PID:g28519
R/Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede,
Eur. J. Biochem. 239, 144-149, 1996
A/Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal an
A/Reference number: S68911; MUID:96305378; PMID:8706699
A/Accession: S68943
A/Molecule type: protein
A/Residues: 84-89, 'E', 91, 145-153, 'A', 155 <VLA>
A/Note: ferritin light chain 1
A/Note: 90-Gly was also found
C/Comment: Ferritin stores iron after its oxidation to the ferric form. It is present in
C/Genetics: GDB:FTL
A/Gene: GDB:FTL

A/Cross-references: GDB:119234; OMIM:134790
A/Map position: 19q13.3-19q13.4
A/Introns: 34/3

A/Note: the list of introns may not be complete
C/Complex: the functional molecule, composed of 24 chains, is roughly spherical with a C
(H) chain (see PIR:FEHJH) and light (L) chain. The predominant chain can be light or he
C/Superfamily: ferritin
C/Keywords: acetylated amino end; iron; metalloprotein; multimer; storage protein
F/2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F/54,57,58,61,64/Binding site: iron (Glu) #status predicted

Query Match 87.9%; Score 756; DB 1; Length 175;
Best Local Similarity 86.2%; Pred. No. 7.4e-57;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLVNLRLASYYTSLGFFYFDRDDVALGVCHEPRELAEKREGAERLLK 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 YSTDVEAAVNSLVNLVTLQASYYTSLGFFYFDRDDVALGVSHPRELAEEKREGYERLLK 68
QY 61 MONRGGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 MONRGGRALFQDIKKPAEDEWGTTPDAMKAAAMALEKKNQALLDLHALGSARTDPHLCD 128
QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVSKAGLGEYLFERLTLKHD 167
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 129 FLETHFLDEEVKLIKMGDHLTNLRHLGPEAGLGEYLFERLTLKHD 175

RESULT 3

JC7238
ferritin protein light chain - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C/Accession: JC7238
R/Cheng, Q.; Gonzalez, P.; Zigler Jr., J-S.
Biochem. Biophys. Res. Commun. 270, 349-355, 2000
A/Title: High level of ferritin light chain mRNA in lens.
A/Reference number: JC7238; MUID:20218664; PMID:10753629
A/Accession: JC7238
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-175 <CHE>
A/Cross-references: UNIPROT:Q9JMK8; GB:AF233445; PIDN:AAF36408.1
A/Experimental source: strain 13/N
C/Comment: This protein is an important regulator of oxidative stress and a primary facto
r responsible for regulating the levels of intracellular iron.
C/Superfamily: ferritin
C/Keywords: iron storage

Query Match 86.6%; Score 745; DB 2; Length 175;
Best Local Similarity 85.6%; Pred. No. 6.3e-56;
Matches 143; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLVNLRLASYYTSLGFFYFDRDDVALGVCHEPRELAEKREGAERLLK 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 YSTEVEAAVNRVLVNLRLQASYYTSLGFFYFDRDDVALAGVGHFRELAKEREKAERLLK 68
QY 61 MONRGGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 MONRGGRALFQDVQKPSSEDEWGTTPDAMEAALTLEKSLNQALLDLHALGSAKTDPHVCD 128
QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVSKAGLGEYLFERLTLKHD 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 129 FLESHFLDEEVKLIKIGDHLTNLRRLDGPQAGLGEYLFERLTLKHD 175

RESULT 4

S01239
ferritin light chain - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C/Accession: S01239
R/Daniels-McQueen, S.; Ray, A.; Walden, W.E.; Ray, B.K.; Brown, P.H.; Thach, R.E.


```
ferritin, tadpole - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C/Accession: A25627
R:/Didbury, J.R.; Theil, E.C.; Kaufman, R.E.; Dickey, L.F.
J. Biol. Chem. 261, 949-955, 1986
A/Title: Multiple red cell ferritin mRNAs, which code for an abundant protein in the emb
A/Reference number: A25627; MUID:86085940; PMID:3484480
A/Accession: A25627
A/Molecule type: mRNA
A/Residues: 1-176 <DID>
A/Cross-references: UNIPROT:P07229; GB:M12120; NID:G213691; PIDN:AAA49532.1; PID:G213692
A/Experimental source: reticulocytes
C/Comment: The sequence of this ferritin is more similar to mammalian H chains than to I
C/Superfamily: ferritin
C/Keywords: erythrocyte; iron storage

Query Match          62.3%; Score 536; DB 1; Length 176;
Best Local Similarity 58.5%; Pred. No. 3e-38;
Matches 96; Conservative 38; Mismatches 30; Indels 0; Gaps 0;

QY      1 YSTEVEAAVNRLVNLTYLRASYTYLISLGFFFRDDVALLEGVCHFFRELAEEKREGGAERLLK 60
       :   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dbd     9 FHRDCEAAINRMVMNNELYASYYTYSMAFYFDRDDIALHNVAKFPEQSHSEERRHAEKLMM 68
       :   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      61 MONQRGGRALFDQLOKPSODEWGTTPDAMKAATYLEKSINQALLDLHALGSKKADPHLCD 120
       ||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dbd     69 DQNKRGGRIVLDVKEPERDEWGNLTLEAMQAALQLEKTVNQALLDLHKVGSDEXDPHLCD 128
       ||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      121 FLSSHFLDEEVKLIKMGDHLTNIQRLVKSKAGLGELYLFERITL 164
       ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dbd     129 FLETYTEEQVSKIKQLGDYITNLKRLGLPQNGMEYILFDKHTM 172
```

RESULT 9
A27805

ferritin chain H - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: A27805

R;Dickey, J.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.
J. Biol. Chem. 262, 7901-7907, 1987

A;Title: Differences in the regulation of messenger RNA for housekeeping and specialized
nification of the first processed pseudogene in amphibia.

A;Reference number: A92648; MUID:87222424; PMID:3495534

A;Accession: A27805

A;Molecule type: mRNA

A;Residues: 1-176 <DIC>

A;Cross-references: UNIPROT:P07229; GB:M15655; NID:g213672; PIDN:AAA49523.1; PID:g213673

C;Superfamily: ferritin

Query Match 62.2%; Score 535; DB 2; Length 176;
Best Local Similarity 58.5%; Pred. No.3.6e-38;
Matches 96; Conservative 38; Mismatches 30; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLNVLYLRASYTYLSLGFYFDRDDVALLEGVCHFFRELAEEKREGAERLLK 60
:
Db 9 FHRDCEAAINRMVMNMELYASYTTLISMAFYFDRDDIALHNVAKFKEQSHERSHAETLMK 68

QY 61 MQNQGRGRLFDLOKPSODEWGTTPDAMKAATVLEKSINQALLDLHALGSKKADPHLCD 120
||:|||||: ||::||: ||||| | :||:|: ||||| ||: ||: ||||| ||:
Db 69 DQNKRGGRIVLDVYKKPERDEWGNLTLEAMQALQLKETVNQALLDLHKVGSKDVPDHLCD 128

QY 121 FLESHFLDEEVKLTKMGDHLTNIQRLVSKAGIGEYLPERLTL 164
||: : : : : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 129 FLETeyLEEQVKSIKQLGDYITNLKRLGLPQNGWGEYLLFDKHTM 172

RESULT 10

FRXL

ferritin heavy chain - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1991 #sequence revision 03-Nov-1995 #text change 09-Jul-2004

```

C;Accession: A37959; S12463; S09499; A40408
R;Holland, L.J.; Wall, A.A.; Bhattacharya, A.
Biochemistry 30, 1965-1972, 1991
A;Title: Xenopus liver ferritin H subunit: cDNA sequence and mRNA production in the liver
A;Reference number: A37959; MUID:91129281; PMID:1993207
A;Accession: A37959
A;Molecule type: mRNA
A;Residues: 1-176 <HOL>
A;Cross-references: UNIPROT:P17663; GB:M55010; NID:g214135; PIDN:AAA49708.1; PID:g214136
A;Experimental source: liver
R;Schoenberg, D.
submitted to the EMBL Data Library, January 1990
A;Reference number: S12463
A;Accession: S12463
A;Molecule type: mRNA
A;Residues: 1-5,'L','7-14','I','16-156','A','159-176 <SCH>
A;Cross-references: EMBL:X51395; NID:g64690; PIDN:CAA35760.1; PID:g64691
R;Moskatis, J.E.; Pastori, R.L.; Schoenberg, D.R.
Nucleic Acids Res. 18, 2184, 1990
A;Title: Sequence of Xenopus laevis ferritin mRNA.
A;Reference number: S09499; MUID:90245677; PMID:2336402
A;Accession: S09499
A;Molecule type: mRNA
A;Residues: 1-5,'L','7-14','I','16-64','70-86','KELKY','87-156','A','159-176 <MOS>
A;Cross-references: EMBL:X51395
A;Note: the sequence shown in the alignment is inconsistent with the nucleotide sequence
R;Muller, J.P.; Vedel, M.; Monnot, M.J.; Touzet, N.; Wegnez, M.
DNA Cell Biol. 10, 571-579, 1991
A;Title: Molecular cloning and expression of ferritin mRNA in heavy metal-poisoned Xenopus
A;Reference number: A40408; MUID:92029619; PMID:1718317
A;Accession: A40408
A;Molecule type: mRNA
A;Residues: 1-9,'H','11-22','M','24-90','G','92-96','T','98-123','AH','126-143','Q','145-176 <MUL>
A;Cross-references: EMBL:X64727
A;Experimental source: cadmium-poisoned XL2 embryonic cell line
C;Complex: The functional molecule is composed of 24 chains, is roughly spherical and con
C;Function:
A;Description: intracellular protein that stores and transports iron in a soluble, nontox
C;Superfamily: ferritin
C;Keywords: iron; iron binding; iron storage; iron transport; metalloprotein; multimer
F;24,58,59,61,62,104/Binding site: iron (Glu, Glu, Glu, Glu, His, Glu) #status predicted
F;81/Binding site: iron (Asp) (shared with tetrameric partners) #status predicted
F;83/Binding site: iron (Lys) (shared with tetrameric partners) #status predicted

Query Match          60.2%; Score 518; DB 1; Length 176;
Best Local Similarity 57.3%; Pred. No. 9.9e-37;
Matches 94; Conservative 37; Mismatches 33; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRILVNLVLRASYTYVLSGFYDRDDVALGVCHFFRELAEKREGAERLLK 60
    :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 9 FNSDCEAALNRMVNLMEYASVYVLSMSYFDRDDVALHHVAKFFKEQSHEEREHAEKFLK 68

QY 61 MONORGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
    ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 69 YQNKRGGRVVLQDIKKPERDEWSNTLEAMQALQLKEKTVNQALLDLHLKASDKVDPQLCD 128

QY 121 FLESHFLDEEVKLIKKMGDHLTNIQRLVKSAGLGEYLFERLTL 164
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 129 FLESEYLEEQVKAMKELGDYITNPKRLGVPQNGMGELYLFDKHTL 172

RESULT 11
C27805
ferritin chain M - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: C27805
R;Dickey, L.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.
J. Biol. Chem. 262, 7901-7907, 1987
A;Title: Differences in the regulation of messenger RNA for housekeeping and specialized
ntification of the first processed pseudogene in amphibia.
A;Reference number: A92648; MUID:87222424; PMID:3495534
A;Accession: C27805

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A;Experimental source: cadmium-poisoned XL2 embryonic cell line
C;Complex: The functional molecule is composed of 24 chains, is roughly spherical and con
C;Function:
A;Description: intracellular protein that stores and transports iron in a soluble, nonoxi
C;Superfamily: ferritin
C;Keywords: iron; iron binding; iron storage; iron transport; metalloprotein; multimer
F;24,58,59,61,62,104/Binding site: iron (Glu, Glu, Glu, Glu, His, Glu) #status predicted
F;81/Binding site: iron (Asp) (shared with tetrameric partners) #status predicted
F;83/Binding site: iron (Lys) (shared with tetrameric partners) #status predicted

Query Match          60.2%;   Score 518;   DB 1;   Length 176;
Best Local Similarity 57.3%;   Pred. No. 9.9e-37;
Matches   94;   Conservative   37;   Mismatches   33;   Indels   0;   Gaps   0;

QY      1 YSTEVEAVNRVLNLYLRASYTISLGFYFDRDDVALEGVCHFFRELAEKREGAERLLK 60
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      9 FNSDCBAINRMVNLNEMYASYYISMSYFFDRDDVALHHVAKFFKEQSHEEREHAEKFLK 68

QY      61 MÖNÖRGGRALFQDLÖKPSÖDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      69 YÖNKRGGRVYLÖDİKKPERDEWSNTLEAMQALÖLEKTVNQALLDLHLKASDKVDPQİCD 128

QY      121 FLESHFIDEEVKLİKKMGDHLTNIQRLVKSAGLGEYLFERLLTL 164
      ||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      129 FLESEYLEEQYKAMKELGDYITNLKRLGVPQNGMGEYLFDKHTL 172

RESULT 11
C27805
ferritin chain M - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: C27805
R;Dickey, L.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.
J. Biol. Chem. 262, 7901-7907, 1987
A;Title: Differences in the regulation of messenger RNA for housekeeping and specialized
ntification of the first processed pseudogene in amphibia.
A;Reference number: A92648; MUID:87222424; PMID:3495534
A;Accession: C27805

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A/Accession: S01948
A/Molecule type: mRNA
A/Residues: 1-182 <M1Y>
A/Cross-references: EMBL:X12812; NID:g50951; PIDN:CAA31300.1; PID:g50952
R/Torti, S.V.; Kwak, E.L.; Miller, S.C.; Miller, L.L.; Ringold, G.M.; Myambo, K.B.; Young, J. Biol. Chem. 263, 12638-12644, 1988
A/Title: The molecular cloning and characterization of murine ferritin heavy chain, a two-chain protein
A/Reference number: A31113; MUID:88315064; PMID:3410854
A/Accession: A31113
A/Molecule type: mRNA
A/Residues: 1-182 <TOR>
A/Cross-references: GB:J03941; NID:g193264; PIDN:AAA37611.1; PID:g309232
R/Beaumont, C.; Dugast, I.; Renaudie, F.; Souroujon, M.; Grandchamp, B. J. Biol. Chem. 264, 7498-7504, 1989
A/Title: Transcriptional regulation of ferritin H and L subunits in adult erythroid and ferritin shells.
A/Reference number: A33355; MUID:89214195; PMID:2708374
A/Accession: A33355
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-16, 'S', 18-136, 'H', 138-139, 'N', 141-163, 'S', 165-182 <BEA>
A/Cross-references: GB:M24509; NID:g193266; PIDN:AAA37612.1; PID:g309233
A/Note: the protein sequence from Fig. 2 is inconsistent with the nucleotide sequence from d 164
C/Genetics:
A/Introns: 38/3; 87/3; 129/3
C/Superfamily: ferritin

Query Match	57.0%	Score 490;	DB 2;	Length 182;
Best Local Similarity	53.0%	Pred. No. 2.4e-34;		
Matches 88;	Conservative 39;	Mismatches 39;	Indels 0;	Gaps 0;

OY	1 YSTEVEAVNRLVNLYL RASYYTSLGFFIEDRDDVALBGCWHFRELAEKREGEARLLK 60
Db	13 YHQAEEAANRQINLELYASYVYLSMSCYFDPRDDVALKNFAKYFLHQSHEREHEAKLMK 72
OY	61 MONORGRALFODLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKADPHLCD 120
Dd	73 LONORGGRIFLODIKKPDRDDWESGLNAMECALHLEKSVNQSLLEHLKLATDKNDPHLCD 132
OY	121 FLESHFLDEEVKLIKMGDHLTNIOQLVKSAGLGLEYLFERLTUKH 166
Dd	133 FIETYYLSEOVKSIKELGDHVTLNRKMGAPEAGNAEYLFCDKHTLGH 178

RESULT 15
FRHUH
ferritin heavy chain - human
N/Alternate names: apoferritin H; ferritin heavy polypeptide 1
C/Species: Homo sapiens (man)
C/Date: 28-Aug-1985 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C/Accession: A23517; A25045; JN0571; A23920; A24844; A03269; A05250; P00562
R/Costanzo, F.; Colombo, M.; Staempfli, S.; Santoro, C.; Marone, M.; Frank, R.; Delius,
Nucleic Acids Res. 14, 721-736, 1986
A/Title: Structure of gene and pseudogenes of human apoferritin H.
A/Reference number: A23517; MUID:86120367; PMID:3003694
A/Accession: A23517
A/Molecule type: DNA
A/Residues: 1-183 <COS>
A/Cross-references: UNIPROT:P02794; GB:X03487; NID:g31340; PIDN:CAA27205.1; PID:g762940;
R/Hentze, M.W.; Keim, S.; Papadopoulos, P.; O'Brien, S.; Modi, W.; Drysdale, J.; Leonarc
Proc. Natl. Acad. Sci. U.S.A. 83, 7226-7230, 1986
A/Title: Cloning, characterization, expression, and chromosomal localization of a human
A/Reference number: A25045; MUID:87016920; PMID:3020541
A/Accession: A25045
A/Molecule type: DNA
A/Residues: 1-183 <HEN>
A/Cross-references: GB:M14211; GB:M14212; NID:g182509; PIDN:AAA52438.1; PID:g182511; GB:
R/Dhar, M.; Chauthaiwale, V.; Joshi, J.G.
Gene 126, 275-278, 1993
A/Title: Sequence of a cDNA encoding the ferritin H-chain from an 11-week-old human fetu
A/Reference number: JN0571; MUID:93246257; PMID:7916709
A/Accession: JN0571

A;Molecule type: mRNA
A;Residues: 1-183 <DHA>
A;Cross-references: GB:M97164; NID:g306743; PIDN:AAA35832.1; PID:g306744
R;Boyd, D.; Vecoli, C.; Belcher, D.M.; Jain, S.K.; Drysdale, J.W.
J. Biol. Chem. 260, 11755-11761, 1985
A;Title: Structural and functional relationships of human ferritin H and L chains deduced from complementary DNA
A;Reference number: A92494; MUID:86008223; PMID:3840162
A;Accession: A23920
A;Molecule type: mRNA
A;Residues: 1-183 <BOY>
A;Cross-references: GB:M11146; NID:g182504; PIDN:AA52437.1; PID:g182505
R;Chou, C.C.; Gatti, R.A.; Fuller, M.L.; Concannon, P.; Wong, A.; Chada, S.; Davis, R.C.,
Mol. Cell. Biol. 6, 566-573, 1986
A;Title: Structure and expression of ferritin genes in a human promyelocytic cell line t(11;17)(p13;p11)
A;Reference number: A93087; MUID:87064341; PMID:3023856
A;Accession: A24844

A;Molecule type: mRNA
A;Residues: 1-183 <CHO>
A;Cross-references: GB:M12937; NID:g182506; PIDN:AAA35830.1; PID:g182507
A;Note: the authors translated the codon CAG for residue 113 as Glu
R;Costanzo, F.; Santoro, C.; Colantuoni, V.; Bensl, G.; Raugeli, G.; Romano, V.; Cortese, EMBO J. 3, 23-27, 1984
A;Title: Cloning and sequencing of a full length cDNA coding for a human apoferritin H c
A;Reference number: A03269; MUID:84158535; PMID:6323167
A;Accession: A03269

A;Molecule type: mRNA
A;Residues: 1-175, 'METVIMKAKPRANP', <CO2>
A;Cross-references: GB:X00318; NID:g28434; PIDN:CA25086.1; PID:g28435
A;Note: this sequence has been revised in reference A23517
R;Luzzago, A.; Felici, F.; Tramontano, A.; Pessi, A.; Cortese, R.
Gene 128, 51-57, 1993

A;Title: Mimicking of discontinuous epitopes by phage-displayed peptides, 1. Epitope map
A;Reference number: PN0562; MUID:93285469; PMID:7685301
A;Contents: annotation; artificial epitopes
R;Lawson, D.M.; Artymiuk, P.J.; Yewdall, S.J.; Smith, J.M.A.; Livingstone, J.C.; Treffry,
Nature 349, 541-544, 1991

A;Title: Solving the structure of human H ferritin by genetically engineering intermolec
A;Reference number: A57130; MUID:91125486; PMID:1992356
A;Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 6-86, 'Q', 88-177
C;Comment: There are several distinct binding sites for iron. Two sites each consist of t
ay bind several iron atoms and possess ferroxidase activity.

C;Genetics:
A;Gene: GDB:FTH1, FTHL6
A;Cross-references: GDB:120617; OMIM:134770

A;Map position: 11q12-11q13
A;Introns: 38/3; 87/3; 129/3

C;Complex: the functional molecule, composed of 24 chains, is roughly spherical with a c(H) chain and light (L) chain (see PIR:FEHUL). The predominant chain can be light or hee

A,Description: intracellular protein that stores and transports iron in a soluble, nontoxic
A,Note: tissues containing high levels of iron and involved in long-term storage tend to
C,Superfamily: ferritin
C,Keywords: iron; iron binding; iron storage; iron transport; metalloprotein; multimer
F,28,62,63,65,66,108/Binding site: iron (Glu, Glu, Glu, His, Glu) #status predicted
F,85/Binding site: iron (Asp) (shared with tetrameric partners) #status experimental
F,87/Binding site: iron (Lys) (shared with tetrameric partners) #status experimental

Query Match	56.6%;	Score 487;	DB 1;	Length 183;
Best Local Similarity	53.0%;	Pred. No. 4.3e-34;		
Matches 87;	Conservative 40;	Mismatches 37;	Indels 0;	Gaps 0;

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QY      1 YSTEVEEAAVNRLVNLYLRSYTYLTLGFPYEDRDVALEGVCHFFRELAEEKGEAERLLK 600
      | : ||| : || | ||| ||| : ||||| ||| : : | : ||| ||| : |
Db     13 YHDSFAAIRQINLELYASYVYLSMSYTFDRDDVALKNFAKFLHQSHHEERHAEKLMK 722
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QY      61 MONORGRALFDLQKPSDEWGTTPDAMKAIVLEKSLNQALLDLHAIGSKKADPHLCD 1200
       :||||||| ||::||| |:: ||: |:: ||::||::||::||| |:: | |||||
Db     73 LONORGRIPLODIKKPCDCDWESGLNAMECALHLEKNVOSLTLEHKLATDKNDPHLCD 1332
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QY      121 FLESHFLDEEVKLIKMGDHLTNIOQLVKSAGLGEYLPERLTJ   164  
       ||::||::|||:||::||||::||::||::||::||::||  
Db     133 FIETHYLENOVKAIKEIGDHVTNLRKMGAPESGLAELYEDKHTJ   176
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Search completed: August 22, 2005, 09:10:52
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:17 ; Search time 42 Seconds
(without alignments)
296.819 Million cell updates/sec

Title: US-10-617-955-2-COPY
Perfect score: 860
Sequence: 1 YSTEVEAAVNRLVNLVLRAS.....VKSAGLGEYLFERLTAKHD 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756	87.9	175	4 US-09-919-039-333	Sequence 333, App
2	731	85.0	238	4 US-09-949-016-10295	Sequence 10295, A
3	487	56.6	220	4 US-09-949-016-10773	Sequence 10773, A
4	334	38.8	250	4 US-09-418-830-2	Sequence 2, Appli
5	334	38.8	250	4 US-09-418-830-3	Sequence 3, Appli
6	256	29.8	243	2 US-08-829-110-3	Sequence 3, Appli
7	221	25.7	107	4 US-09-621-976-4402	Sequence 4402, Ap
8	146	17.0	168	3 US-09-134-001C-4664	Sequence 4664, Ap
9	94	10.9	162	4 US-09-602-777A-362	Sequence 362, App
10	88	10.2	175	4 US-09-489-039A-14335	Sequence 14335, A
11	83.5	9.7	644	3 US-09-300-909-18	Sequence 18, Appl
12	82.5	9.6	168	4 US-09-543-681A-7822	Sequence 7822, Ap
13	82	9.5	998	4 US-09-198-452A-841	Sequence 841, App
14	82	9.5	998	4 US-09-438-185A-793	Sequence 793, App
15	80.5	9.4	629	3 US-09-300-909-19	Sequence 19, Appl
16	80	9.3	277	4 US-09-602-777A-8	Sequence 8, Appli
17	80	9.3	514	4 US-09-902-540-10406	Sequence 10406, A
18	79	9.2	719	4 US-09-763-902B-5	Sequence 5, Appli
19	77.5	9.0	390	4 US-09-107-532A-6425	Sequence 6425, Ap
20	77.5	9.0	482	4 US-09-902-540-16249	Sequence 16249, A
21	77.5	9.0	502	4 US-09-949-016-7837	Sequence 7837, Ap
22	77	9.0	302	4 US-09-270-767-59138	Sequence 59138, A
23	77	9.0	501	4 US-09-270-767-43743	Sequence 43743, A
24	76.5	8.9	491	4 US-09-248-796A-19312	Sequence 19312, A
25	76	8.8	7831	4 US-09-902-540-12902	Sequence 12902, A
26	75	8.7	374	4 US-09-710-279-1562	Sequence 1562, Ap
27	75	8.7	397	3 US-09-134-001C-4104	Sequence 4104, Ap

28	75	8.7	610	4 US-09-252-991A-19594	Sequence 19594, A
29	74	8.6	397	4 US-09-252-991A-24798	Sequence 24798, A
30	74	8.6	3433	4 US-09-091-501B-10	Sequence 10, Appl
31	74	8.6	3433	4 US-09-538-092-1136	Sequence 1136, Ap
32	73.5	8.5	163	4 US-09-489-039A-10135	Sequence 10135, A
33	73.5	8.5	173	3 US-08-818-112-82	Sequence 82, Appl
34	73.5	8.5	173	3 US-08-818-112-83	Sequence 83, Appl
35	73.5	8.5	173	3 US-09-056-556-82	Sequence 82, Appl
36	73.5	8.5	173	4 US-09-072-596-83	Sequence 83, Appl
37	73.5	8.5	173	4 US-09-072-967-82	Sequence 82, Appl
38	73.5	8.5	181	4 US-09-050-739-54	Sequence 54, Appl
39	73.5	8.5	208	4 US-09-489-039A-12447	Sequence 12447, A
40	73	8.5	314	4 US-09-252-991A-27913	Sequence 27913, A
41	73	8.5	1074	4 US-09-902-540-10427	Sequence 10427, A
42	73	8.5	1114	4 US-09-902-540-16251	Sequence 16251, A
43	72.5	8.4	414	1 US-08-002-202-13	Sequence 13, Appl
44	72.5	8.4	414	1 US-08-002-202-17	Sequence 17, Appl
45	72.5	8.4	414	1 US-08-002-202-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-919-039-333
; Sequence 333, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919, 039
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222, 113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 333
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 4005778CD1
US-09-919-039-333

Query Match 87.9%; Score 756; DB 4; Length 175;
Best Local Similarity 86.2%; Pred. No. 9.6e-73;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASVTVSLGFFPDRDVALEGVCHFFRELAEEKREGARLLK 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 YSTDVEAAVNSLVNLVLAQASYTVSLGFFPDRDVALEGVSHFFRELAEEKREGYERLLK 68
QY 61 MONQGRALFQDLQKPSQDEWGTTPDAMKAATVEKSLNQALLDLHALGSKADPHLCD 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 MONQGRALFQDIKKPADEWGTTPDAMKAAMALEKLNQALLDLHALGSAARTDPHLCD 128
QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTAKHD 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGGPEAGLGEYLFERLTAKHD 175

RESULT 2
US-09-949-016-10295
; Sequence 10295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10295
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10295
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Query Match      85.0%; Score 731; DB 4; Length 238;
Best Local Similarity 84.3%; Pred. No. 6.8e-70;
Matches 140; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
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QY 1 YSTEVEAAVNRVLNLYLRASYTYLSLGFYFDRDDVALGVCCHFFRELAEEKREGAERLLK 60
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Db 72 YSTDVEAAVNSLVNLYLQASYYTSLSLGFYFDRDDALEGVSHFFRELTEEEKREGYERLLK 131
QY 61 MONQGRGALFQDLQKPSDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 132 MONQGRGALFQDIKKPAEDWGTTPDAMKAAMALEKKLNQALLDLHALDSAHMDPHLCD 191
QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLKH 166
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 192 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLKH 237
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RESULT 3
US-09-949-016-10773
; Sequence 10773, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10773
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10773
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Query Match      56.6%; Score 487; DB 4; Length 220;
Best Local Similarity 53.0%; Pred. No. 6.4e-44;
Matches 87; Conservative 40; Mismatches 37; Indels 0; Gaps 0;
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QY 1 YSTEVEAAVNRVLNLYLRASYTYLSLGFYFDRDDVALGVCCHFFRELAEEKREGAERLLK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 50 YHQDSEAAINRQINLVLASYVYLSMSYFDRDDVALKNFAKYFLHQSHREERHAELMK 109
QY 61 MONQGRGALFQDLQKPSDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 110 LQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKQVNSLLELHKLATDKNDPHLCD 169
QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLKH 164
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 170 FIETHYLNQVAKIKELGDHVTNLKRMGAPESGLAETLFDKHTL 213
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RESULT 4
US-09-418-830-2
; Sequence 2, Application US/09418830
; Patent No. 6563019
; GENERAL INFORMATION:
; APPLICANT: Deak, Maria
; APPLICANT: Dudits, Denes
; APPLICANT: Torok, Karolyne
; APPLICANT: Sass, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-418-830-2
```

```
Query Match      38.8%; Score 334; DB 4; Length 250;
Best Local Similarity 42.4%; Pred. No. 1.6e-27;
Matches 72; Conservative 38; Mismatches 52; Indels 8; Gaps 3;
```

```
QY 1 YSTEVEAAVNRVLNLYLRASYTYLSLGFYFDRDDVALGVCCHFFRELAEEKREGAERLLK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 YQDEVESAINQINVEYNVSYYVHSLFAFYFDRDNVALKGLAKFFKSSSEEREHAELMK 144
QY 61 MONQGRGALFQDLQKPSOD---EWGTPDAMKAIVLEKSLNQALLDLHALGSKKADP 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 145 YQNRGGRVLAHPVSPSEFDDHAEGDALYAMEIALSLEKLVNEKLVNHSVADRNDP 204
QY 117 HLCDFLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLKH 166
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 205 QLANFIESEFLVEQVESIKKISEYVTQLRLVGK--GHGVWHFDQ-TLLH 250
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```
RESULT 5
US-09-418-830-3
; Sequence 3, Application US/09418830
; Patent No. 6563019
; GENERAL INFORMATION:
; APPLICANT: Deak, Maria
; APPLICANT: Dudits, Denes
; APPLICANT: Torok, Karolyne
; APPLICANT: Sass, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
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115-08-829-110-3

US-09-134-001C-460

US-09-134-001C-460

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Query Match          17.0%; Score 146; DB 3; Length 168;
Best Local Similarity 25.5%; Pred. No. 1e-07;
Matches      42; Conservative    40; Mismatches   67; Indels    16; Gaps     5,
QY              STEVEA VNR L VNLYLRAS YTYLSLGFYDRDVALEGVCHPFRRLAEKREGAERLLKM 61
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB             5 SKELLALNEQMNGEYFAAHAYMAAAYCDKE--SYDGAFANFYIEQAKEERFHGKKIYDY 62
QY            QNQRGRALLFODLQKPSODEWGTTPDAMKAIVLEKSINQALIDLHALGSKADPHLCDF 121
| || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB           63 INDRGEHAIFDTIKAP-KVEFSILLETFKDSLQGERDVTOGRFYNLSELARNDKYATISF 121
QY          122 LESHFLDEBEVKLIKMGDLTNIQRLVYSKAGLGE-----YLFEER 161
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB         122 L-NWFLDEQVEESTFTETHIDYLTR-----IGDDCNTLYLYEK 158

RESULT 9
US-09-602-777A-362
; Sequence 362, Application US/09602777A
; Patent No. 6831165
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habermayer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128CP
; CURRENT APPLICATION NUMBER: US/09/602,777A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932924.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9

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; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; SEQ ID NO 362
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-362

Query Match      10.9%; Score 94; DB 4; Length 162;
Best Local Similarity 22.1%; Pred. No. 0.034;
Matches 34; Conservative 38; Mismatches 72; Indels 10; Gaps 4;

QY      4 EVEAAVNRLVNLIRASYTYLSTGFYFDRDDVALGVCHEFFRELAEEKREGAERLLKMQN 63
        : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      6 KIASAFNNQVTAELEASMVYLQLSYL--DDLGLTGRMDWMKAQSKEELEHAQKFAQHLL 63

QY      64 QRGGRALFDLDQKPSODEWGTTPDMAKCAIVLEKSINQALLDLHALGSKKAD---PHLCD 120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      64 DRDYPQIGDIAPPKLDVTSAI-EAPEASLAHQKISGLIRELAIAIQDAEKDYDSRALID 122

QY      121 FLESHFLDEEVKLIKMGDHLTNIOQLVSKAGL 154
        : |||::: ::::: ||:
DB      123 W---FLNEQIEEATVGIIIDLRIAGDSGSGI 152

RESULT 10
US-09-489-039A-14335
; Sequence 14335, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14335
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14335

Query Match      10.2%; Score 88; DB 4; Length 175;
Best Local Similarity 22.4%; Pred. No. 0.16;
Matches 36; Conservative 29; Mismatches 86; Indels 10; Gaps 4;

QY      3 TEVEAAVNRLVNLILRASYYLSLGTFYFDRDDVALGVCHEFFRELAEEKREGAERLLKMQ 62
        |:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      14 TDMIDKLNQNMNLELYSSLLYQQMSAWCSYH--SPEGAAAFIRRHQAQEEMTHMQRLFYDL 71

QY      63 NORGGRAFQDLQKPSODEWGTTPDMAKCAIVLEKSINQALLDLHALGSKKADPHLCDPL 122
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      72 TDGTSLPRINAIASPFA-EYASLDELFRQTYEHQQLITQKINELAHAAMTSQDYPTFNFL 130

QY      123 ESHFLD--EEVKLIKMGDHLTNIOQLVSKAGLGEYLFER 161
        : : : | | | | | | | | | | | | | | | | | | | | | |
DB      131 QMVAEQHEEEKLFKSVIDKLT-----LAGKSGEGLYFIDK 166

RESULT 11
US-09-300-909-18
; Sequence 18, Application US/09300909
```


; Patent No. 6306580
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING
; TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,909
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/083,942
; FILING DATE: 01-MAY-1998
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 644 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-300-909-18

Query Match	9.7%	Score 83.5	DB 3	Length 644
Best Local Similarity	21.9%	Pred. No. 3		
Matches	28	Conservative 22	Mismatches 55	Indels 23
			Gaps 2	
QY	60	KM Q N O R G G R A L F O D L Q K P S O D E W G T T P D A M K A I V E K S I N G A L L D H A L G S K K A D P H L C	119	
		::	::	::
Db	304	K L R S Q T C A L Y W F R T A M S N I S D V O G T T P E W I D R L T V L Q H S F N D N I F D S E W V Q W A Y D N E L T	363	
QY	120	D-----F L E S H F L D E E V K L I K K M G D H L T N I Q R L V K S K A G L G E Y L F	159	
		::	::	::
Db	364	D D S D I A Y Y Y A Q L A D S N S N A A F L K S ---N S Q A K I V K D C G I M C R H Y K K A E K R K M S I G Q W I Q	420	
QY	160	E R L T L K H D	167	
		::		
Db	421	S R C E K T N D	428	

```

RESULT 12
US-09-543-681A-7822
; Sequence 7822, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7822
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7822

```

	Query Match	9.6%	Score 82.5;	DB 4;	Length 168;
	Best Local Similarity	23.2%;	Pred No.0.6;		
	Matches	32;	Conservative	24;	Mismatches 77; Indels 5; Gaps 3;
QY	9 VNRLVNLYL RAS YTYL SLGFYEDRDVALLEGVC HFFRELAEEKREGAERLLKMQNORGR	68	:	:	:
Dd	11 LNEQLNLEFY SANLYLQMSAWC--DDKGFDGA AKFLKAHSRREMEHMQR LFDYLSDTGAM	68	:	:	:
QY	69 ALFQDLQKPSQDEWGTTPDAMIKAIVLEKSLNQALLDLHALGSKKADPHLCDFLESHPLD	128	:	:	:

Db 69 PLIGTIEAPPA-EFLSLSDLFTKTYEHEKFTAEINKLAHLAMTTQDYSTFNELQWVAE 127

Qy 129 --EEVKLTKKMGDHLTNI 144
|| || | : | | :
128 QHEEKLFXSILDKLAMV 145

Db

```

RESULT 13
US-09-198-452A-841
; Sequence 841, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 841
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-841

```

Query Match	9.5%	Score 82	DB 4	Length 998
Best Local Similarity	24.1%	Pred. No. 7.9		
Matches	34	Conservative 17	Mismatches 50	Indels 40
			Gaps 5	
QY	12	LVNLYLRASYTYLISLGF---	YFDRDDVA-----	LEGVCHFFRELAEKREGAER 57
		:	: :	: :
Db	328	LIHYQLQESTVRAIFPKBGLFSKEQVAFSTQHPRELSEIQRVYHYLHAYEEAK-----		381
QY	58	LLKMQNORGRALFQDLQKPSQDEWGTTPDAMKAATVLEKSINQALLDLH--		ALGSKKA 114
Db	382	-----SAFIHDTQNPULLKAMEYTLATLADA-----		SQPTISNHIRLALGWKSE 424
QY	115	DPHLCDFLFESHFLDEEVKLTK		135
			: : :	:
Db	425	DPHSLVSLVTHFVEEEVENIR		445

```

RESULT 14
; US-09-438-185A-793
; Sequence 793, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalmann, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 793
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0791
; US-09-438-185A-793

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Query Match	9.5%;	Score 82;	DB 4;	Length 998;
Best Local Similarity	24.1%;	Pred. No.	7.9;	

Matches 34; Conservative 17; Mismatches 50; Indels 40; Gaps 5;

QY 12 LVNLYLRASYTYLSLGF---YFDRDDVA-----LEGVCHFFRELAERKREGAER 57

Db 328 LHHYQLQESTVRAIFFEKGLFSKEQVAFSTQHPRELSIQRVYHYLHAYEEAK----- 381

QY 58 LKMQNQRGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLH--ALGSKKA 114

Db 382 -----SAFIHDTQNPPLKAMEYTLATLADA-----SQPTISNHIRLALGWKSE 424

QY 115 DPHLCDFLSHFLDEEVKLIK 135

Db 425 DPHSLVSLVTHFVEEVENIR 445

RESULT 15

US-09-300-909-19

; Sequence 19, Application US/09300909

; Patent No. 6306580

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING

; TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR

; NUMBER OF SEQUENCES: 27

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/300, 909

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/083,942

; FILING DATE: 01-MAY-1998

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 629 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-300-909-19

Query Match 9.4%; Score 80.5; DB 3; length 629;

Best Local Similarity 21.6%; Pred. No. 6.1;

Matches 22; Conservative 20; Mismatches 37; Indels 23; Gaps 2;

QY 80 DEMGTPDAMKAIVLEKSLNQALLDLHALGS-----KKADPHLC 119

Db 311 DVGTEPWEIERQTVLQHSFNDDTTPDLQMVQWQAYNDVMDSEIAYKYAQLADSDSNAC 370

QY 120 DFLESHFLDEEVKLIKMGDHLTNIQRLVKSKAGLGEYLFER 161

Db 371 AFLKS--NSQAKIVKDCGTMCRHYKRAEKRQMSMGQWIKSR 409

Search completed: August 22, 2005, 09:07:09

Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:18 ; Search time 1065 Seconds
(without alignments)
61.404 Million cell updates/sec

Title: US-10-617-955-2-COPY
Perfect score: 860
Sequence: 1 YSTEVEAAVNRLVNLRLRAS.....VKSAGLGEYLFERLTAKHD 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues
Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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19:	/cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	850	98.8	167	US-10-617-955-4	Sequence 4, Appli
2	849	98.7	167	US-10-617-955-2	Sequence 2, Appli
3	839	97.6	175	US-10-042-865-174	Sequence 174, App
4	799	92.9	167	US-10-142-8388-2	Sequence 2, Appli
5	756	87.9	175	US-09-919-039-333	Sequence 333, App
6	756	87.9	175	US-10-435-666-4	Sequence 4, Appli
7	756	87.9	175	US-10-262-445-56	Sequence 56, Appli
8	756	87.9	175	US-10-734-564-128	Sequence 128, App
9	756	87.9	175	US-10-684-742-14	Sequence 14, Appli
10	756	87.9	175	US-10-489-740-144	Sequence 144, App
11	756	87.9	254	US-10-104-047-3198	Sequence 3198, Ap

12	738	85.8	175	15	US-10-042-865-171	Sequence 171, App
13	738	85.8	175	17	US-10-732-923-5089	Sequence 5089, Ap
14	731	85.0	175	15	US-10-042-865-172	Sequence 172, App
15	730	84.9	183	15	US-10-042-865-173	Sequence 173, App
16	728	84.7	199	16	US-10-363-829-400	Sequence 400, App
17	726	84.4	183	15	US-10-384-496-14	Sequence 14, Appli
18	721	83.8	183	15	US-10-384-496-10	Sequence 10, Appli
19	721	83.8	183	15	US-10-042-865-175	Sequence 175, App
20	712	82.8	183	15	US-10-384-496-8	Sequence 8, Appli
21	709	82.4	191	16	US-10-684-742-2	Sequence 2, Appli
22	673	78.3	160	17	US-10-732-923-5087	Sequence 5087, Ap
23	654	76.0	154	14	US-10-029-386-29603	Sequence 29603, A
24	548	63.7	148	9	US-09-864-761-39398	Sequence 39398, A
25	493	57.3	181	18	US-10-617-316-174	Sequence 174, App
26	492	57.2	180	14	US-10-324-153-4	Sequence 4, Appli
27	492	57.2	182	15	US-10-384-496-12	Sequence 12, Appli
28	490	57.0	182	15	US-10-384-496-6	Sequence 6, Appli
29	490	57.0	182	18	US-10-220-335-238	Sequence 238, App
30	487	56.6	183	15	US-10-384-496-2	Sequence 2, Appli
31	487	56.6	183	17	US-10-734-049A-231	Sequence 231, App
32	483	56.2	190	15	US-10-435-666-8	Sequence 8, Appli
33	483	56.2	190	16	US-10-734-564-127	Sequence 127, App
34	481	55.9	164	17	US-10-732-923-5088	Sequence 5088, Ap
35	472.5	54.9	184	16	US-10-425-115-197075	Sequence 197075,
36	469	54.5	173	15	US-10-216-464-29	Sequence 29, Appli
37	469	54.5	242	14	US-10-324-153-2	Sequence 2, Appli
38	468.5	54.5	175	17	US-10-732-923-5079	Sequence 5079, Ap
39	439.5	51.1	171	17	US-10-732-923-5077	Sequence 5077, Ap
40	436	50.7	99	16	US-10-425-115-189990	Sequence 189990,
41	434	50.5	181	17	US-10-732-923-5086	Sequence 5086, Ap
42	431	50.1	149	17	US-10-732-923-5085	Sequence 5085, Ap
43	425	49.4	101	16	US-10-425-115-207417	Sequence 207417,
44	420	48.8	183	9	US-09-801-574-70	Sequence 70, Appli
45	419.5	48.8	172	17	US-10-732-923-4972	Sequence 4972, Ap

ALIGNMENTS

RESULT 1
US-10-617-955-4 Application US/10617955
; Sequence 4, Appli
; Publication No. US20040142164A1
; GENERAL INFORMATION:
; APPLICANT: Matsushita Electric Industrial Co., Ltd.
; TITLE OF INVENTION: FINE PARTICLE FILM AND PRODUCING METHOD OF THE SAME
; FILE REFERENCE: 061352-0039
; CURRENT APPLICATION NUMBER: US/10/617,955
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: PCT/JP02/11954
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 2001-343526
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Liver of Apoferritin of Equus caballus
US-10-617-955-4

Query Match 98.8%; Score 850; DB 16; Length 167;
Best Local Similarity 98.8%; Pred. No. 2.9e-81;
Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1 YSTEVEAAVNRLVNLRLRASYYTSLGFFPRDDVALEGVCHFFRELAEEKRGAEERLLK 60
Db 1 YSTEVEAAVNRLVNLRLRASYYTSLGFFPRDDVALEGVCHFFRELAEEKRGAEERLLK 60
CY 61 MONRGGRALFDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120

```
Db      61  M0N0RGGRALF0DL0KPS0DEWGTTPDAMKAIVLEKSLN0ALLDLHALGSAQADPHLCD 120
QY      121  FLESHFLDEEVKLIKMGDHLTNIOQLVSKAGLGEYLFERLTLKHD 167
Db      121  FLESHFLDEEVKLIKMGDHLTNIOQLVSKAGLGEYLFERLTLKHD 167
```

RESULT 2

```
US-10-617-955-2
; Sequence 2, Application US/10617955
; Publication No. US20040142164A1
; GENERAL INFORMATION:
; APPLICANT: Matsushita Electric Industrial Co., Ltd.
; APPLICANT: Yamashita, Ichiro
; TITLE OF INVENTION: FINE PARTICLE FILM AND PRODUCING METHOD OF THE SAME
; FILE REFERENCE: 061352-0039
; CURRENT APPLICATION NUMBER: US/10/617,955
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: PCT/JP02/11954
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 2001-343526
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Liver Apoferritin of Equus caballus
US-10-617-955-2
```

```
Query Match      98.7%; Score 849; DB 16; Length 167;
Best Local Similarity 98.8%; Pred. No. 3.6e-81;
Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1  YSTEVEAAVNRVLNLYLRASYTYLSLGFYFDRDDVALLEGVCHFFRELAEEKREGAERLLK 60
Db      1  YSTEVEAAVNRVLNLYLRASYTYLSLGFYFDRDDVALLEGVCHFFRELAEEKREGAERLLK 60
QY      61  M0N0RGGRALF0DL0KPS0DEWGTTPDAMKAIVLEKSLN0ALLDLHALGSKKADPHLCD 120
Db      61  M0N0RGGRALF0DL0KPS0DEWGTTPDAMKAIVLEKSLN0ALLDLHALGSKKADPHLCD 120
QY      121  FLESHFLDEEVKLIKMGDHLTNIOQLVSKAGLGEYLFERLTLKHD 167
Db      121  FLESHFLDEEVKLIKMGDHLTNIOQLVSKAGLGEYLFERLTLKHD 167
```

RESULT 3

```
US-10-042-865-174
; Sequence 174, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
```

```
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-042-865-174

Query Match      97.6%; Score 839; DB 15; Length 175;
Best Local Similarity 97.6%; Pred. No. 4.4e-80;
Matches 163; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1  YSTEVEAAVNRVLNLYLRASYTYLSLGFYFDRDDVALLEGVCHFFRELAEEKREGAERLLK 60
Db      9  YSTEVEAAVNRVLNLYLRASYTYLSLGFYFDRDDVALLEGVCHFFRELAEEKREGAERLLK 68
QY      61  M0N0RGGRALF0DL0KPS0DEWGTTPDAMKAIVLEKSLN0ALLDLHALGSKKADPHLCD 120
Db      69  M0N0RGGRALF0DL0KPS0DEWGTTPDAMKAIVLEKSLN0ALLDLHALGSAQADPHLCD 128
QY      121  FLESHFLDEEVKLIKMGDHLTNIOQLVSKAGLGEYLFERLTLKHD 167
Db      129  FLESHFLDEEVKLIKMGDHLTNIOQLVSKAGLGEYLFERLTLKHD 175
```

RESULT 4

```
US-10-142-838B-2
; Sequence 2, Application US/10142838B
; Publication No. US20030124741A1
; GENERAL INFORMATION:
; APPLICANT: Matsushita Electric Industrial Co., Ltd.
; TITLE OF INVENTION: Recombinant cage-like protein, Method for producing the same,
; TITLE OF INVENTION: Precious metal-recombinant cage-like protein complex, Method for
; TITLE OF INVENTION: producing the same and recombinant DNA
; FILE REFERENCE: Apoferritin DNA PRT
; CURRENT APPLICATION NUMBER: US/10/142,838B
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: JP P2001-142983
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant Liver Apoferritin
```

prev. Filed 4/18/01

per para 2, 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100


```

; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining prior application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CuraSeqIst version 0.1
; SEQ ID NO 56
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-445-56

```

```

Query Match      87.9%; Score 756; DB 15; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.5e-71;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

```

```

Qy      1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALEGVCHFRELAEKREGAERLLK 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      9 YSTDVEAAVNSLVNLVYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEKREGYERLLK 68
Qy      61 MONORGRALFQDLQPSODEWGTTTPDAMKAATVLEKSLNQALLDLHALGSKKADPHLCD 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      69 MONORGRALFQDIKKPAEDWGTTPDAMKAAMALEKKNQALLDLHALGSAKRTDPHLCD 128
Qy      121 FLESHFLDEEVKLIKMGDHLTNIQRLVSKAGLGEYLFERLTLKHD 167
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      129 FLETHFLDEEVKLIKMGDHLTNLHRLGSPREALGEYLFERLTLKHD 175

```

```

RESULT 8
US-10-734-564-128
; Sequence 128, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using TIMP1
; FILE REFERENCE: 1657/2012
; CURRENT APPLICATION NUMBER: US/10/734,564
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-564-128

```

```

Query Match      87.9%; Score 756; DB 16; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.5e-71;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
Qy      1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALEGVCHFRELAEKREGAERLLK 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

Db      9 YSTDVEAAVNSLVNLVYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEKREGYERLLK 68
Qy      61 MONORGRALFQDLQPSODEWGTTTPDAMKAATVLEKSLNQALLDLHALGSKKADPHLCD 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      69 MONORGRALFQDIKKPAEDWGTTPDAMKAAMALEKKNQALLDLHALGSAKRTDPHLCD 128
Qy      121 FLESHFLDEEVKLIKMGDHLTNIQRLVSKAGLGEYLFERLTLKHD 167
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      129 FLETHFLDEEVKLIKMGDHLTNLHRLGSPREALGEYLFERLTLKHD 175

```

```

RESULT 9
US-10-684-742-14
; Sequence 14, Application US/10684742
; Publication No. US20040259107A1
; GENERAL INFORMATION:
; APPLICANT: Bernardino Ghetti
; TITLE OF INVENTION: FERRITIN LIGHT SUBUNIT VARIANT-ENCODING
; TITLE OF INVENTION: NUCLEIC ACIDS, POLYPEPTIDES, TANGENIC ANIMALS COMPRISING
; TITLE OF INVENTION: THE SAME, ANTIBODIES THERETO, AND METHODS OF USE THEREOF
; FILE REFERENCE: ARTI 0253
; CURRENT APPLICATION NUMBER: US/10/684,742
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/418,126
; PRIOR FILING DATE: 2003-10-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-684-742-14

```

```

Query Match      87.9%; Score 756; DB 16; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.5e-71;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

```

```

Qy      1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALEGVCHFRELAEKREGAERLLK 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      9 YSTDVEAAVNSLVNLVYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEKREGYERLLK 68
Qy      61 MONORGRALFQDLQPSODEWGTTTPDAMKAATVLEKSLNQALLDLHALGSKKADPHLCD 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      69 MONORGRALFQDIKKPAEDWGTTPDAMKAAMALEKKNQALLDLHALGSAKRTDPHLCD 128
Qy      121 FLESHFLDEEVKLIKMGDHLTNIQRLVSKAGLGEYLFERLTLKHD 167
      |||:|||||:|||||:|||||:|||||:|||||:|||||
Db      129 FLETHFLDEEVKLIKMGDHLTNLHRLGSPREALGEYLFERLTLKHD 175

```

```

RESULT 10
US-10-489-740-144
; Sequence 144, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: P9
; FILE REFERENCE: Angiogenesis_PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 144
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-740-144

```

```

Query Match      87.9%; Score 756; DB 17; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.5e-71;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

```

```
QY 1 YSTEVEAAVNRLVNLIRASYTYLSLGFYFDRDDVALGVCHFFRELAEEKREGAERLLK 60
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 YSTDVEAAVNSLVNLVLIQASYTYLSLGFYFDRDDVALGVSHFFRELAEEKREGYERLLK 68
QY 61 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 MONORGGRALFQDIKKPAEDWCKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCD 128
QY 121 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFERLTLKHD 167
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLKHD 175

RESULT 11
US-10-104-047-3198
; Sequence 3198, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3198
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3198
```

```
Query Match      87.9%; Score 756; DB 15; Length 254;
Best Local Similarity 86.2%; Pred. No. 4e-71;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 1 YSTEVEAAVNRLVNLIRASYTYLSLGFYFDRDDVALGVCHFFRELAEEKREGAERLLK 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 88 YSTDVEAAVNSLVNLVLIQASYTYLSLGFYFDRDDVALGVSHFFRELAEEKREGYERLLK 147
QY 61 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 148 MONORGGRALFQDIKKPAEDWCKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCD 207
QY 121 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFERLTLKHD 167
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 208 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLKHD 254
```

```
RESULT 12
US-10-042-865-171
; Sequence 171, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patuturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grose, William M
; APPLICANT: Alsbrook II, John P
```

```
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-042-865-171
```

```
Query Match      85.8%; Score 738; DB 15; Length 175;
Best Local Similarity 83.8%; Pred. No. 1.9e-69;
Matches 140; Conservative 15; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 1 YSTEVEAAVNRLVNLIRASYTYLSLGFYFDRDDVALGVCHFFRELAEEKREGAERLLK 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 YSTEVEAAVNRLVNLVNLIRASYTYLSLGFYFDRDDVALGVSHFFRELAEEKREGAERLLK 68
QY 61 MONORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 LONORGGRALFLDVQKPSQDEWCKTQDAMEAALLVERLNQALLDLHGLASARGDPHICD 128
QY 121 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFERLTLKHD 167
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 FLEHFLDEEVKLIKMGDHLTNLRLLAGPQAGLGEYLFERLTLKHD 175
```

```
RESULT 13
US-10-732-923-5089
; Sequence 5089, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 5089
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-732-923-5089
```

```
Query Match      85.8%; Score 738; DB 17; Length 175;
Best Local Similarity 85.6%; Pred. No. 1.9e-69;
Matches 143; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
```

```
OY 1 YSTEVEAAVNRLVNLYLRASTYTLISLGFYFDRDDVALBEGVCHFFRELAEEKREGAERLLK 60
Db 9 YSPEVEAAVNHLVNLHLRASYTYLSLGFYFDRDDVALBEGVSHFFRELAEEKREAERLLK 68
OY 61 MONORGRALFODLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
Db 69 MONORGRALFQDVQKPSQDEWGTTLNAMEAALALEKNIQALLDLHALGSAHTDPHLCD 128
OY 121 FLESHFLDEEVKLIKKGMDHLTNIOQLVKSAGLGEYLFERLTLKHD 167
Db 129 FLENHFLDEEVKLIKKGMDHLTNIRLSGPQASLGEYLFERLTLKHD 175
```

RESULT 14

```
US-10-042-865-172
; Sequence 172, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; PRIOR APPLICATION DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 172
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-10-042-865-172
```

Query Match 85.0%; Score 731; DB 15; Length 175;
Best Local Similarity 84.4%; Pred. No. 1.1e-68;

```
Matches 141; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
OY 1 YSTEVEAAVNRLVNLYLRASTYTLISLGFYFDRDDVALBEGVCHFFRELAEEKREGAERLLK 60
Db 9 YSTEVEAAVNRLVNLHLQASYTYLSLGFYFDRDDVALAGVGHFFRELAEEKREGAERLLK 68
OY 61 MONORGRALFODLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
Db 69 TONORGRALFQDVQKPSQDEWGTTLNAMEAALTLKSLNQALLDLHALGSAKTSVHCD 128
OY 121 FLESHFLDEEVKLIKKGMDHLTNIOQLVKSAGLGEYLFERLTLKHD 167
Db 129 FLENHFLDEEVKLIKKGMDHLTNIRLDGPQAGLGEYLFERLTLKHD 175
```

RESULT 15

```
US-10-042-865-173
; Sequence 173, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; PRIOR APPLICATION DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 173
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-042-865-173
```

Query Match 84.9%; Score 730; DB 15; Length 183;

Best Local Similarity 81.7%; Pred. No. 1.4e-68;
Matches 143; Conservative 15; Mismatches 9; Indels 8; Gaps 1;

```
QY      1 YSTEVEAAVNRLVNIYLIRASYTYLSLGFYFDRDDVALLGVCHFFRELAEEKREGAERLLK 60
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      9 YSTEVEAAVNRLVNIHLIRASYTYLSLGFYFDRDDVALLGVGHFFRELAEEKREGAERLLK 68

QY      61 MONQGGGRLFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
          :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      69 LQNERGGGRLFQDVQKPSQDEWGTTPDAMKALLLEKNLQALLDLHALGSAQADPHLCD 128

QY      121 FLESHFLDEEVKLIKMGDHLTNIQ-----LVKSKAGLGELYLFEHLTILKHD 167
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      129 FLESHFLDKEVKLIKMGHNLTNLRWQGPQPAQTGVAQASLGELYLFEHLTILKHD 183
```

Search completed: August 22, 2005, 09:28:43
Job time : 1066 secs

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Matches	156;	Conservative	5;	Mismatches	6;	Indels	0;	Gaps	0
Qy	1	YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCHFFRELAEEKREGAERLLK	60						
Db	1	YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCHFFRELAEEKREGAERLLK	60						
Qy	61	MONORGGRALFQDLQKPSQDEMGTTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHL	120						
Db	61	MONORGGRALFQDLQKPSQDEMGTTTPDAMKAAIVLEKSLNQALLDLHALGSAQADPHL	120						
Qy	121	FLESHFLDEEVKLIKMGDHLTNIQRLVKSKAGLGEYLFERLT	167						
Db	121	FLSSHFLDEEVKLIKMGDHLTNIQRLVGSQAGLGEYLFERLT	167						
RESULT 4									
ID	ABR64209	standard; protein; 175 AA.							
AC	ABR64209;								
DT	15-OCT-2003	(first entry)							
DE	Angiogenesis protein BNO103.								
KW	Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;								
KW	antipsoriatic; antiarteriosclerotic; cardiact; vasotropic; angiogenesis;								
KW	gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;								
KW	diabetic retinopathy; cardiovascular disease; atherosclerosis;								
KW	ischemic limb disease; coronary artery disease.								
OS	Homo sapiens.								
XX	PN	WO2003027285-A1.							
XX	PD	03-APR-2003.							
XX	PF	19-SEP-2002; 2002WO-AU001282.							
XX	PR	27-SEP-2001; 2001AU-00007973.							
XX	PR	27-SEP-2001; 2001AU-00007974.							
XX	PR	11-OCT-2001; 2001AU-00008210.							
XX	PR	29-OCT-2001; 2001AU-00008532.							
XX	PR	13-NOV-2001; 2001AU-00008838.							
XX	PR	28-AUG-2002; 2002AU-00951032.							
XX	PA	(BION-) BIONOMICS LTD.							
XX	PI	Gamble JR, Hahn CN, Vadas MA;							
XX	DR	WPI; 2003-354655/33.							
XX	DR	N-PSDB; ACP34484.							
XX	PT	New angiogenic genes and polypeptides, useful for diagnosing,							
XX	PT	prognosticating or treating an angiogenesis-related disorder, e.g.							
XX	PT	cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or							
XX	PT	cardiovascular diseases.							
XX	PS	Claim 15; SEQ ID NO 144; 90pp; English.							
XX	CC	The invention relates to the isolation of novel genes (ACR34446-ACF34559)							
XX	CC	encoding proteins (ABR64180-ABR64281) involved in the process of							
XX	CC	angiogenesis. The nucleic acid molecules are useful in identifying and/or							
XX	CC	obtaining full-length human genes involved in an angiogenic process. The							
XX	CC	nucleic acid molecule, polypeptides or complexes encoded, cells or							
XX	CC	genetically modified non-human animals derived from these are useful for							
XX	CC	the screening of candidate pharmaceutical compounds used in treating							
XX	CC	angiogenesis-related disorders. They are also useful for diagnosing,							
XX	CC	prognosticating or treating an angiogenesis-related disorder, which							
XX	CC	involves uncontrolled or enhanced angiogenesis or is a disorder in which							
XX	CC	a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,							
XX	CC	diabetic retinopathy, psoriasis or cardiovascular diseases such as							
XX	CC	atherosclerosis), or involves inappropriately arrested or decreased							

Query Match	87.9%;	Score 756;	DB 6;	Length 175;
Best Local Similarity	86.2%;	Pred. No. 2.4e-70;		
Matches 144;	Conservative 11;	Mismatches 12;	Indels 0;	Gaps 0;
QY	1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCHFFRELAEKREGAERLLK 60			
DB	9 YSTDVEAAVNSLVNLVYLQASLYTSLGFFYFDRDDVALGVSHFFRELAEKREGYERLLK 68			
QY	61 MONRGGRALLFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120			
DB	69 MONRGGRALLFQDIKKPAEDWGTTPDAMKAAMALEKSLNQALLDLHALGSAKADPHLCD 128			
QY	121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLLKHD 167			
DB	129 FLETHFLDEEVKLIKMGDHLTNLRLGPEAGLGEYLFERLTLLKHD 175			
RESULT 5				
ID	ABU89807	standard; protein; 175 AA.		
XX	AC	ABU89807;		
XX	DT	10-JUL-2003 (first entry)		
XX	DE	Novel human protein NOV18c.		
XX	KW	Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer; NOV.		
OS	XX	Homo sapiens.		
XX	PN	WO2003031571-A2.		
XX	PD	17-APR-2003.		
PF	02-OCT-2002;	2002WO-US031357.		
XX	05-OCT-2001;	2001US-0327454P.		
PR	09-OCT-2001;	2001US-0327917P.		
PR	09-OCT-2001;	2001US-0328029P.		
PR	09-OCT-2001;	2001US-0328056P.		
PR	12-OCT-2001;	2001US-0328849P.		
PR	15-OCT-2001;	2001US-0329414P.		
PR	17-OCT-2001;	2001US-0330142P.		
PR	22-OCT-2001;	2001US-0341058P.		
PR	24-OCT-2001;	2001US-0343629P.		
PR	29-OCT-2001;	2001US-0349575P.		
PR	01-NOV-2001;	2001US-0346357P.		
PR	25-JUN-2002;	2002US-0391342P.		
PR	01-OCT-2002;	2002US-00262445.		
PA	(CURA-)	CURAGEN CORP.		
PI	Alsbrook JP,	Burgess CE, Catterton E, Chant JS, Chaudhuri A;		
PI	Edinger SR,	Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;		
PI	Mezes PS,	Miller I, Ooi CE, Patturajan M, Rieger DK, Spytek KA;		
PI	Taupier RJ,	Zerhusen BD, Zhong H, Zhong M;		
DR	WPI,	2003-381704/36.		
DR	N-PSDB;	ACA90184.		
PT	New DAPK3 polypeptide,	useful for preparing a composition for treating or		
PT	preventing e.g., cancer.			

PS Claim 2; Page 141; 253pp; English.
XX The invention describes an isolated polypeptide comprising any of 33 90-
CC 1273 amino acid sequences (I) given in the specification or its mature
CC form, a sequence that is at least 95 % identical to (I), or a sequence
CC comprising one or more conservative substitutions in the amino acid
CC sequence of (I). The polypeptide is useful for preparing a composition
CC for treating or preventing e.g. cancer. This is the amino acid sequence
CC of a novel human NOV protein
XX
SQ Sequence 175 AA;

Query Match 87.9%; Score 756; DB 6; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.4e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALBGVCHFFRELAEEKREGAERLLK 60
||:||||| ||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 YSTDVEAAVNSLVNLVLRQASYTYLSLGFYFDRDDVALBGVSHFFRELAEEKREGYERLLK 68

QY 61 MONRGGRALFQDLQKPSODEWGTPDAMKAATVLEKSLNQALLDLHALGSKKADPHLCD 120
||||||| ||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 MONRGGRALFQDIKKPAEDWGKTPDAMKAAMTLEKLNQALLDLHALGSARTDPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLKHD 167
||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGGPEAGLGEYLFERLTLKHD 175

RESULT 6
ADG42356
ID ADG42356 standard; peptide; 175 AA.
XX
AC ADG42356;
XX
DT 26-FEB-2004 (first entry)
XX
XX
DE Ferritin L chain for HIV tat peptide-ferritin L chain fusion protein.
XX
XX anti-HIV; virucide; vaccine; gene therapy; ferritin; fusion protein;
KW polymeric assembly; AIDS; SARS; oxygen transport; blood substitute;
KW image contrast agent; metal chelating agent; gelling agents;
KW protein purification platform.
XX
OS Homo sapiens.
XX
PN WO2003094849-A2.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-US014617.
XX
PR 10-MAY-2002; 2002US-0379145P.
XX
PA (NEWC-) NEW CENTURY PHARM INC.
XX
PI Carter DC, Li CQ;
XX
DR WPI; 2003-903936/82.
XX
XX
PT New ferritin fusion proteins in which ferritin is fused with a protein
PT capable of being fused to ferritin without interfering with polymeric
PT assembly of resulting fusion protein, useful as human or veterinary
PT vaccines and therapeutics.
XX
XX
PS Example 3; SEQ ID NO 4; 52pp; English.
XX
CC The invention relates to a ferritin fusion protein comprising a fusion
CC protein selected from a ferritin protein fused at the C-terminus or at
CC the N-terminus with a protein or peptide capable of being fused to
CC ferritin without interfering with the polymeric assembly of the resulting
CC fusion protein. The fusion proteins are useful in the development of
CC human and veterinary vaccines and therapeutics against e.g. AIDS or SARS,

CC or in other applications including oxygen transport and the therapeutic
CC delivery of drugs and other therapeutic agents, or as blood substitutes,
CC image contrast agents, metal chelating agents, gelling agents, protein
CC purification platforms, and therapeutic receptor-binding proteins. In an
CC example of the invention, a peptide from the HIV Tat protein is fused to
CC the N-terminus of the ferritin L chain via a 6 Gly spacer. This peptide
CC represents the ferritin L chain which is fused to the HIV Tat peptide.
XX
SQ Sequence 175 AA;

Query Match 87.9%; Score 756; DB 7; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.4e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALBGVCHFFRELAEEKREGAERLLK 60
||:||||| ||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 YSTDVEAAVNSLVNLVLRQASYTYLSLGFYFDRDDVALBGVSHFFRELAEEKREGYERLLK 68

QY 61 MONRGGRALFQDLQKPSODEWGTPDAMKAATVLEKSLNQALLDLHALGSKKADPHLCD 120
||||||| ||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 MONRGGRALFQDIKKPAEDWGKTPDAMKAAMALEKLNQALLDLHALGSARTDPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLKHD 167
||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGGPEAGLGEYLFERLTLKHD 175

RESULT 7
ADE77168
ID ADE77168 standard; protein; 175 AA.
XX
AC ADE77168;
XX
DT 29-JAN-2004 (first entry)
XX
XX
DE Human protein expressed in a liver disorder #85.
XX
XX human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
KW tumour; liver; inflammatory disorder; immune response disorder;
KW high-throughput screening; differential gene expression; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003108871-A1.
XX
PD 12-JUN-2003.
XX
PF 30-JUL-2001; 2001US-00919039.
XX
PR 28-JUL-2000; 2000US-0222113P.
XX
PA (KASE/) KASER M R.
XX
PI Kaser MR;
XX
DR WPI; 2004-031227/03.
DR N-PSDB; ADE77167.
XX
XX
PT Composition comprising several cDNAs that are differentially expressed in
PT treated human C3A liver cell cultures, useful for treating liver
PT disorders.
XX
XX
PS Claim 1; SEQ ID NO 333; 41pp; English.
XX
CC The invention relates to a composition comprising several cDNAs that are
CC differentially expressed in a liver disorder. The composition is useful
CC for treating liver disorder such as hyperlipidaemia, hypertension, type
CC II diabetes, tumours of the liver and disorders of the inflammatory and
CC immune response. The composition is useful for a high-throughput method
CC of screening several molecules or compounds to identify a ligand which
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC high-throughput method for using a protein to screen several molecules or
CC compounds to identify at least one ligand which specifically binds the

CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficacy of treatment. The present sequence represents the amino acid
CC sequence of a protein encoded by a cDNA differentially expressed in a
CC liver disorder.
XX
SQ Sequence 175 AA;

Query Match 87.9%; Score 756; DB 8; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.4e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALEGVCHFRELAEKREGAERLLK 60
||:||||| |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 YSTDVEAAVNSLVNLVYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEKREGYERLLK 68

QY 61 MONORGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 MONORGRALFQDIKKPAEDWGKTPDAMKAMALEKLNQALLDLHALGSARTDPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLTKHD 167
||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLTKHD 175

RESULT 8

ID ADN11575
ADN11575 standard; protein; 175 AA.

AC ADN11575;

DT 15-JUL-2004 (first entry)

DE Human wild-type ferritin light chain protein.

KW neuroprotective; neurodegenerative disease; FTL;
KW ferritin light chain variant; iron deposition; human.

OS Homo sapiens.

PN WO2004033661-A2.

PD 22-APR-2004.

PF 14-OCT-2003; 2003WO-US032412.

PR 11-OCT-2002; 2002US-0418126P.

PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

PI Vidal R, Ghatti B;

DR WPI; 2004-340922/31.

DR N-PSDB; ADN11574.

XX New isolated polynucleotide encoding ferritin light chain variant
PT polypeptide, useful for treating diseases related to aberrant ferritin
PT and/or iron deposition which affect other organ systems, or
PT neurodegenerative diseases.

PS Example 1; Fig 7B; 107pp; English.

CC The present invention provides the protein and coding sequences of a
CC human ferritin light chain variant polypeptide. The nucleic acid encoding
CC ferritin light chain variant polypeptide, the polypeptides and antibodies
CC are useful as research tools to examine the role of ferritin light
CC polypeptide (FTL) in the development of neurodegenerative disease,
CC identify binding partners of FTL variant polypeptides, identify signaling

CC pathways which regulate FTL variant expression, and screen for and
CC characterize agents capable of modulating FTL variant activity. The
CC nucleic acids can also be used as probes to detect the presence of and/or
CC expression of genes encoding FTL variant-like proteins. It can also be
CC used to create recombinant cell lines for use in assays to identify
CC agents, which modulate FTL variant mediated regulation of aberrant
CC ferritin and iron deposition. Agents capable of modulating FTL variant
CC activity are useful for treating diseases related to aberrant ferritin
CC and/or iron deposition which affect other organ systems, and
CC neurodegenerative diseases. The present sequence is the human wild-type
CC FTL protein.
XX
SQ Sequence 175 AA;

Query Match 87.9%; Score 756; DB 8; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.4e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALEGVCHFRELAEKREGAERLLK 60
||:||||| |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 YSTDVEAAVNSLVNLVYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEKREGYERLLK 68

QY 61 MONORGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 MONORGRALFQDIKKPAEDWGKTPDAMKAMALEKLNQALLDLHALGSARTDPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLTKHD 167
||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLTKHD 175

RESULT 9

ID ADQ26090
ADQ26090 standard; protein; 175 AA.

AC ADQ26090;

DT 23-SEP-2004 (first entry)

DE Light polypeptide ferritin.

XX BCEC; brain capillary endothelial cell; astrocyte; permeability;
KW endothelial cell; pro-barrier; PB;
KW microvascular permeability-modifying disorder;
KW neurodegenerative disorder; cerebrovascular accident;
KW Alzheimer's disease; vascular-related dementia;
KW Creutzfeldt-Jacob disease; bovine spongiform encephalopathy;
KW Parkinson's disease; brain trauma; multiple sclerosis;
KW peripheral disorder; septic shock; hepatic encephalopathy;
KW diabetic hypertension; diabetic microangiopathy; sleeping sickness;
KW neuropsychiatric disorder; depression; autism; schizophrenia; psychosis;
KW CNS disorder; brain tumor; epilepsy; migraine; narcolepsy; insomnia;
KW chronic fatigue syndrome; mountain sickness; AIDS-related dementia;
KW angio genesis-related disorder; proliferative vitreoretinopathy;
KW rheumatoid arthritis; Crohn's disease; atherosclerosis;
KW ovarian hyperstimulation; psoriasis; endometriosis; neovascularisation;
KW restenosis; balloon angioplasty; scar tissue overproduction;
KW peripheral vascular disease; hypertension; inflammatory vasculitides;
KW Reynaud's disease; Reynaud's phenomenon; aneurysm; arterial restenosis;
KW thrombophlebitis; lymphangitis; lymphedema; wound healing; tissue repair;
KW ischaemia reperfusion injury; angina; myocardial infarction;
KW chronic heart condition; osteoporosis; Light polypeptide ferritin; FTL.

OS Homo sapiens.

PN WO2004056386-A2.

PD 08-JUL-2004.

PF 19-DEC-2003; 2003WO-NL000915.
PR 19-DEC-2002; 2002EP-00080503.
PR 25-APR-2003; 2003US-0465234P.

XX (UYLE-) RIJKSUNIV LEIDEN.
PA
XX
PI Gaillard PJ, De Boer AG, Brink A;
XX
DR WPI; 2004-500264/47.
XX
PT Modulating the permeability of endothelial cells, useful for treating or
PT preventing e.g. neurodegenerative disorders, comprises altering in the
PT endothelial cells the activity or the steady-state level of a pro-barrier
PT polypeptide.
XX
PS Claim 1; SEQ ID NO 44; 222pp; English.

XX This sequence represents light polypeptide ferritin encoded by the FTL
CC gene. This protein is upregulated in BCEC (brain capillary endothelial
CC cells) by physical co-culture with astrocytes. This protein sequence may
CC be used in the method of the invention for modulating the permeability of
CC endothelial cells. The method comprises altering in the endothelial cells
CC the activity or the steady-state level of a pro-barrier (PB) polypeptide
CC having an amino acid sequence selected from ADQ26047ADQ26048ADQ26049ADQ26050ADQ2605
CC 1ADQ26052ADQ26053ADQ26054ADQ26055ADQ26056ADQ26057ADQ26058ADQ26059ADQ26060
CC ADQ26061ADQ26062ADQ26063ADQ26064ADQ26065ADQ26066ADQ26067ADQ26068ADQ26069A
CC DQ26070ADQ26071ADQ26072ADQ26073ADQ26074ADQ26075ADQ26076ADQ26077ADQ26078AD
CC Q26079ADQ26080ADQ26081ADQ26082ADQ26083ADQ26084ADQ26085ADQ26086ADQ26087ADQ
CC 26088ADQ26089ADQ26090ADQ26091ADQ26092ADQ26093ADQ26094ADQ26095ADQ26096ADQ2
CC 6097ADQ26098ADQ26099. The PB polypeptides, nucleic acid molecules
CC encoding them, antagonists or a gene therapy vector comprising an
CC antisense nucleotide sequence capable of inhibiting the expression of the
CC nucleotide sequence encoding a PB polypeptide, are useful in the
CC manufacture of a composition for treating or preventing a microvascular
CC permeability-modifying disorder, including neurodegenerative disorders
CC (e.g. cerebrovascular accidents, Alzheimer's disease, vascular-related
CC dementia, Creutzfeldt-Jacob disease, bovine spongiform encephalopathy,
CC Parkinson's disease, brain trauma, multiple sclerosis), peripheral
CC disorders with a CNS component (such as septic shock, hepatic
CC encephalopathy, (diabetic) hypertension, diabetic microangiopathy or
CC sleeping sickness), neuropsychiatric disorders (e.g. depression, autism,
CC schizophrenia and other psychoses; other CNS disorders (brain tumours,
CC epilepsy, migraine, narcolepsy, insomnia, chronic fatigue syndrome,
CC mountain sickness, or AIDS-related dementia); and angiogenesis-related
CC disorders (proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's
CC disease, atherosclerosis, ovarian hyperstimulation, psoriasis,
CC endometriosis associated with neovascularisation, restenosis subsequent
CC to balloon angioplasty, scar tissue overproduction, peripheral vascular
CC disease, hypertension, inflammatory vasculitides, Reynaud's disease,
CC Reynaud's phenomenon, aneurysms, arterial restenosis, thromboplebitis,
CC lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
CC reperfusion injury, angina, myocardial infarctions, chronic heart
CC conditions, or osteoporosis). The PB polypeptide may also be used in the
CC manufacture of a composition for reversibly increasing the microvascular
CC permeability in a subject.

XX Sequence 175 AA;

Query Match 87.9%; Score 756; DB 8; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.4e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVYLRASTYTLISLGFYFDRDDVALLEGVCHFFRELAEEKREGAERLLK 60
Db 9 YSTDVEAAVNSLVNLVYLQASYYTLISLGFYFDRDDVALLEGVSHFFRELAEEKREGYERLLK 68
QY 61 MÖNÖRGGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
Db 69 MÖNÖRGGRALFQDIKKPADEWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCD 128
QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLKHD 167
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLKHD 175

RESULT 10
ADQ29702
ID ADQ29702 standard; protein; 175 AA.
XX
AC ADQ29702;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human colorectal cancer-associated protein #57.
XX
KW human; colon cancer; TIMP1; Reg1-alpha;
KW colorectal cancer-associated marker.
XX
OS Homo sapiens.
XX
PN EP1439393-A2.
XX
PD 21-JUL-2004.
XX
PF 15-DEC-2003; 2003EP-00257868.
XX
PR 13-DEC-2002; 2002US-0433554P.
PR 31-JUL-2003; 2003US-0491397P.
XX
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PI Astle JH, Boardman LA, Bugart LJ, Burgess CC, Catino TJ;
PI Dwivedi P, Huntress M, Johnson KA, Lewis ME, Maimonis PJ, Myerow SH;
PI Brown-Shimer SLA, Thiagalingam A, Thibodeau SN, Molino GA;
XX
DR WPI; 2004-545561/53.
DR N-PSDB; ADQ29635.
XX

PT Diagnosing colon cancer in individual, preferably human, by detecting
PT presence of TIMP 1 in sample, where presence of TIMP 1 in sample is
PT indicative of colon cancer in individual.

XX Claim 7; SEQ ID NO 128; 433pp; English.

XX The invention comprises a method for diagnosing colon cancer in an
CC individual, the method involves obtaining a serum sample from the
CC individual and detecting the presence of either TIMP1 or Reg1-alpha and
CC an additional colorectal cancer-associated marker. The method of the
CC invention is useful for diagnosing colon cancer in an individual. The
CC present amino acid sequence represents a human colorectal cancer-
CC associated protein of the invention.

XX Sequence 175 AA;

Query Match 87.9%; Score 756; DB 8; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.4e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVYLRASTYTLISLGFYFDRDDVALLEGVCHFFRELAEEKREGAERLLK 60
Db 9 YSTDVEAAVNSLVNLVYLQASYYTLISLGFYFDRDDVALLEGVSHFFRELAEEKREGYERLLK 68
QY 61 MÖNÖRGGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
Db 69 MÖNÖRGGRALFQDIKKPADEWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCD 128
QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTLKHD 167
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLKHD 175

RESULT 11
ABM82153
ID ABM82153 standard; protein; 175 AA.
XX
AC ABM82153;
XX

DT	18-NOV-2004	(first entry)	
XX			
DE	Tumour-associated antigenic target (TAT) polypeptide PRO71085, SEQ:5563.		
KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer;		
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;		
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;		
KW	central nervous system cancer; bladder cancer; pancreatic cancer;		
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;		
KW	chromosome identification; chromosome mapping; gene mapping;		
KW	gene therapy; cytostatic.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2004030615-A2.		
XX			
PD	15-APR-2004.		
XX			
PF	29-SEP-2003; 2003WO-US028547.		
XX			
PR	02-OCT-2002; 2002US-0414971P.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Wu TD, Zhang Z, Zhou Y;		
XX			
DR	WPI, 2004-347921/32.		
XX			
DR	N-PSDB; ACN40653.		
XX			
PT	New tumor-associated antigenic target polypeptides and nucleic acids,		
PT	useful in preparing a medicament for treating or detecting a		
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or		
PT	prostate cancer or tumor.		
XX			
PS	Claim 12; SEQ ID NO 5563; 7273bp; English.		
XX			
CC	The invention relates to human tumour-associated antigenic target (TAT)		
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are		
CC	overexpressed in cancer tissues compared to normal tissues, and may thus		
CC	serve as effective targets for the diagnosis and treatment of cancer in		
CC	mammals. The invention also relates to nucleic acid and polypeptide		
CC	sequences at least 80% identical to the TAT nucleic acid and		
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic		
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic		
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a		
CC	TAT polypeptide; and methods and compositions for the treatment or		
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,		
CC	antibodies, antagonists, binding molecules and compositions are useful		
CC	for diagnosing or treating a cell proliferative disorder associated with		
CC	increased TAT expression, particularly cancers such as breast cancer,		
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder		
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central		
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be		
CC	used as hybridisation probes, in chromosome and gene mapping, in		
CC	chromosome identification and in gene therapy. The present sequence		
CC	represents a TAT polypeptide of the invention		
XX			
SQ	Sequence 175 AA;		
QY	Query Match	87.9%; Score 756; DB 8; Length 175;	
	Best Local Similarity	86.2%; Pred. No. 2.4e-70;	
	Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0		
Db	1 YSTEVEA VNR L VNL YLRAS YTYL SLGFY PDRD VAL EGVCH FPRE LAE KREGA ERLLK 60		
	9 YSTDEA VAVNS L VNL YLQAS YTYL SLGFY PDRD VAL EGVSH FPRE LAE KREGY ERLLK 68		
QY	61 MONORGG RAL FOD LQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120		
	69 MONORGG RAL FOD IKKPAEDWGTTPDAMKAMALEKSLNQALLDLHALGSA RDPHLCD 128		
QY	121 FLESHFLDEEVKLIKMGDHLTNIQRLVSKSKAGLGEYLFERLT LKHD 167		

```

Db          129 FLETHFLDEEVKLIKMGDHLTNLHRLGGPEAGLGYYLFFERLTLKHD 175

RESULT 12
ADB65044
ID      ADB65044 standard; protein; 254 AA.
XX
AC      ADB65044;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Human protein encoded by clone SMINT20016150.
XX
KW      Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW      cell regeneration; membrane protein; signal transduction-related protein;
KW      transcription-related protein; osteoporosis; neurological disease;
KW      cancer; tumour.
XX
OS      Homo sapiens.
XX
PN      EP1308459-A2.
XX
PD      07-MAY-2003.
XX
PF      28-MAR-2002; 2002EP-00007401.
XX
PI      05-NOV-2001; 2001JP-00379298.
PR      25-JAN-2002; 2002US-00350978.
XX
PA      (HELI-) HELIX RES INST.
PA      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI      Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI      Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI      Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
WPI: 2003-450961/43.
DR      N-PSDB; ADB63074.
XX
PT      New polynucleotides and polypeptides, useful for developing a diagnostic
PT      marker or medicines for regulation of their expression and activity, or
PT      as targets of gene therapy.
XX
PS      Claim 1; Page; 222pp; English.
XX
CC      The invention discloses a polynucleotide comprising a sequence selected
CC      from 1970 fully defined nucleotide sequences which encode novel
CC      polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC      or its partial peptide, an antibody binding to the polypeptide or peptide
CC      of the polynucleotide, immunologically assaying the polypeptide or peptide
CC      peptide of the polynucleotide by contacting the polypeptide or peptide
CC      with the antibody of the encoded protein, and observing the binding
CC      between the two, a transformant carrying the polynucleotide in an
CC      expressible manner and an antisense polynucleotide. The oligonucleotide
CC      is useful as a primer for synthesising the polynucleotide, or as a probe
CC      for detecting the polynucleotide. The polynucleotides and encoded
CC      proteins are useful as pharmaceutical agents and many disease-related
CC      genes may be included in them, for developing a diagnostic marker or
CC      medicines for regulation of their expression and activity, or as targets
CC      of gene therapy. The genes are involved in tissue and/or cell
CC      regeneration. Membrane proteins, signal transduction-related proteins,
CC      transcription-related proteins, disease-related proteins and genes
CC      encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC      neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC      the activity or expression of the encoded protein to treat diseases. The
CC      sequence presented is a protein of the invention. Note: Some of the
CC      sequence data for this patent is not represented in the printed
CC      specification, but is based on sequence information supplied by the
CC      European Patent Office.
XX
SQ      Sequence 254 AA;

```

Best Local Similarity 86.2%; Pred. No. 4e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYSLSGFYFDRDDVALEGVCHFFRELAEEKREGAERLLK 60
|||:|||||
Db 88 YSTDVEAAVNSLVNLVLRASYTYSLSGFYFDRDDVALEGVSHFFRELAEEKREGYERLLK 147
QY 61 MONORGGRALFQDLQKPSODEWGTTTPDAMKAATVLEKSLNQALLDLHALGSKKADPHLCD 120
|||:|||||
Db 148 MONORGGRALFQDIKKPAEDEWGKTTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCD 207
QY 121 FLESHFLDEEVKLKKMGDHLTNIQRLVSKAGLGELYFERLLTKHD 167
|||:|||||
Db 208 FLETHFLDEEVKLKKMGDHLTNLHRLGGPEAGLGELYFERLLTKHD 254

RESULT 13

ADQ82746
ID ADQ82746 standard; protein; 362 AA.
XX
AC ADQ82746;
XX
DT 09-SEP-2004 (first entry)
XX
DE Recombinant human ferritin protein.
XX
KW human; ferritin protein.
XX
OS Homo sapiens.
XX
PN KR2004007892-A.
XX
PD 28-JAN-2004.
XX
PF 11-JUL-2002; 2002KR-00040497.
XX
PR 11-JUL-2002; 2002KR-00040497.
XX
PA (BIOP-) BIOPROGEN CO LTD.
XX
PI Ham MS, Jung BH, Kim SU, Lee EG, Lee JW;
XX
DR WPI; 2004-386312/36.
DR N-PSDB; ADQ82747.
XX
PT New recombinant human ferritin proteins and production method of them.
XX
PS Claim 8; SEQ ID NO 11; 27pp; Korean.
XX
CC The invention comprises the amino acid and coding sequences of a
CC recombinant human ferritin protein, the invention also comprises a
CC production method for the recombinant human ferritin protein. The present
CC amino acid sequence represents the recombinant human ferritin protein of
CC the invention.
XX
SQ Sequence 362 AA;

Query Match 87.9%; Score 756; DB 8; Length 362;
Best Local Similarity 86.2%; Pred. No. 6.2e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYSLSGFYFDRDDVALEGVCHFFRELAEEKREGAERLLK 60
|||:|||||
Db 196 YSTDVEAAVNSLVNLVLRASYTYSLSGFYFDRDDVALEGVSHFFRELAEEKREGYERLLK 255
QY 61 MONORGGRALFQDLQKPSODEWGTTTPDAMKAATVLEKSLNQALLDLHALGSKKADPHLCD 120
|||:|||||
Db 256 MONORGGRALFQDIKKPAEDEWGKTTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCD 315
QY 121 FLESHFLDEEVKLKKMGDHLTNIQRLVSKAGLGELYFERLLTKHD 167
|||:|||||
Db 316 FLETHFLDEEVKLKKMGDHLTNLHRLGGPEAGLGELYFERLLTKHD 362

RESULT 14

AAU29923
ID AAU29923 standard; protein; 238 AA.
XX
AC AAU29923;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #414.
XX

KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX

OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX

Nucleic acids encoding a range of human polypeptides, useful in genetic
vaccination, testing and therapy.

Claim 20; Page 210; 765pp; English.

XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 238 AA;

Query Match 87.6%; Score 753; DB 4; Length 238;
Best Local Similarity 85.6%; Pred. No. 7.5e-70;
Matches 143; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYSLSGFYFDRDDVALEGVCHFFRELAEEKREGAERLLK 60
|||:|||||
Db 72 YSTDVEAAVNSLVNLVLRASYTYSLSGFYFDRDDVALEGVSHFFRELAEEKREGYERLLR 131
QY 61 MONORGGRALFQDLQKPSODEWGTTTPDAMKAATVLEKSLNQALLDLHALGSKKADPHLCD 120
|||:|||||
Db 132 MONORGGRALFQDIKKPAEDEWGKTTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCD 191
QY 121 FLESHFLDEEVKLKKMGDHLTNIQRLVSKAGLGELYFERLLTKHD 167
|||:|||||
Db 192 FLETHFLDEEVKLKKMGDHLTNLHRLGGPEAGLGELYFERLLTKHD 238

RESULT 15

ADO60419

ID ADO60419 standard; protein; 175 AA.

XX ADO60419;

AC ADO60419;

XX 26-AUG-2004 (first entry)

DT 26-AUG-2004 (first entry)

XX Human ferritin light chain to increase B lymphocyte proliferation.

DE Human ferritin light chain to increase B lymphocyte proliferation.

XX B lymphocyte proliferation; differentiation; maturation; ferritin;

KW diagnosis; HIV infection; lymphoma.

XX Homo sapiens.

OS Homo sapiens.

XX WO2004045561-A2.

PN WO2004045561-A2.

XX 03-JUN-2004.

PD 03-JUN-2004.

XX 20-NOV-2003; 2003WO-US037593.

PF 20-NOV-2003; 2003WO-US037593.

XX 20-NOV-2002; 2002US-0427754P.

PR 20-NOV-2002; 2002US-0427754P.

XX (UYMA-) UNIV MASSACHUSETTS.

PA (UYMA-) UNIV MASSACHUSETTS.

XX Stevenson M, Swingler S;

PI Stevenson M, Swingler S;

XX WPI; 2004-431807/40.

DR WPI; 2004-431807/40.

XX Inducing B cell proliferation, differentiation or maturation for treating

PT HIV infection or cancer, comprises administering ferritin or a compound

PT that increases ferritin expression or activity to the B cell or its

PT precursor cell.

XX Example 1; SEQ ID NO 1; 86pp; English.

PS Example 1; SEQ ID NO 1; 86pp; English.

XX The invention relates to a method of increasing at least one of B

CC lymphocyte proliferation, differentiation or maturation, by administering

CC ferritin or a compound that increases ferritin expression or activity to

CC a B lymphocyte or a B lymphocyte precursor cell in an amount to increase

CC B lymphocyte proliferation, differentiation or maturation. The methods

CC are useful for modulating B lymphocyte proliferation, differentiation or

CC maturation, or for identifying compounds that modulate ferritin

CC expression or activity. These may be used for treating or diagnosing HIV

CC infection or lymphoma. This sequence corresponds to the human ferritin

CC light chain protein used in the method of the invention.

XX Sequence 175 AA;

SQ Sequence 175 AA;

Query Match 86.3%; Score 742; DB 8; Length 175;
Best Local Similarity 85.0%; Pred. No. 7e-69;
Matches 142; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

Qy 1 YSTEVEAAVNRLLVNLVLRASYTYLSLGFYFDRDDVALGVCFFPRELAEBKREGAERLLK 60
Db 9 YSTDVEAAVNSLVNLVLRASYTYLSLGFYFDRDDVALGVCFFPRELAEBKREGYERLLK 68

Qy 61 MONORGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
Db 69 MONORGVRLAFQDLQKPAEDWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 128

Qy 121 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGYYLFFERLTLKHD 167
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGYYLFFERLTLKHD 175

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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:17 ; Search time 172 Seconds
(without alignments)
497.193 Million cell updates/sec

Title: US-10-617-955-2-COPY
Perfect score: 860
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	839	97.6	174	1 FRIL_HORSE	P02791 equus caball
2	756	87.9	174	1 FRIL_HUMAN	P02792 homo sapien
3	756	87.9	241	2 Q7Z2W1	Q7z2w1 homo sapien
4	752	87.4	175	2 Q6IBT7	Q6ibc7 homo sapien
5	750	87.2	175	2 Q96AU9	Q96au9 homo sapien
6	748	87.0	175	2 Q96CU0	Q96cu0 homo sapien
7	747	86.9	175	2 Q8WT07	Q8wu07 homo sapien
8	745	86.6	175	2 Q86WT9	Q86w19 homo sapien
9	745	86.6	175	2 Q9JKN8	Q9jkm8 cavia porce
10	738	85.8	174	1 FRIL_BOVIN	Q46415 bos taurus
11	738	85.8	174	1 FRIL_RABIT	P09451 oryctolagus
12	731	85.0	175	2 Q9BYW6	Q9byw6 homo sapien
13	731	85.0	175	2 Q9UKP6	Q9jxp6 cavia porce
14	728	84.7	183	2 Q6P7T1	P02793 rattus norv
15	726	84.4	182	1 FRIL_RAT	P49945 mus musculu
16	721	83.8	182	1 FRIL_MOUSE	P29391 mus muscu
17	716	83.3	183	2 Q9CPX4	Q9cpw0 xenopus lae
18	712	82.8	182	1 FRIL_MOUSE	P29391 mus musculu
19	712	82.8	183	2 Q66GW0	Q66gw0 xenopus lae
20	709	82.4	191	2 Q6S4P3	Q6s4p3 homo sapien
21	673	78.3	160	2 Q9GLE7	Q9gle7 sus scrofa
22	595.5	69.2	1310	2 Q7TP54	Q7tp54 rattus norv
23	538	62.6	178	2 Q6PAN0	Q6pan0 xenopus tro
24	536	62.3	176	2 Q6P8C6	Q6p8c6 xenopus tro
25	535	62.2	176	1 FRIL_RANCA	P07229 rana catesb
26	534	62.1	178	2 Q7ZWM3	Q7zwm3 xenopus lae
27	532	61.9	173	2 Q6DFP5	Q6dfp5 xenopus tro
28	530	61.6	177	1 FRIL_XENLA	Q7sxa5 xenopus lae
29	529	61.5	177	2 Q80IJ5	Q80ij5 petromyzon
30	528	61.4	176	2 Q6PAB7	Q6pab7 xenopus lae
31	526	61.2	177	2 Q6PG53	Q6pg53 xenopus lae

32	523	60.8	176	2 P79821	P79821 oncorhynch
33	521	60.6	176	2 P79823	P79823 oncorhynch
34	520	60.5	176	2 P79822	P79822 oncorhynch
35	518	60.2	176	1 FRH1_XENLA	P17663 xenopus lae
36	516	60.0	176	1 PRIM_SALSA	P49947 salmo salar
37	514	59.8	176	1 FRH2_XENLA	P49948 xenopus lae
38	513	59.7	176	1 FR12_RANCA	P07798 rana catesb
39	498	57.9	177	2 Q6DDB5	Q6ddb5 xenopus tro
40	498	57.9	177	2 Q9DDT0	Q9ddt0 brachydanio
41	498	57.9	182	2 Q920K4	Q920k4 cavia porce
42	497	57.8	177	2 Q7ZXM8	Q7zxm8 xenopus lae
43	497	57.8	182	2 Q8MIP0	Q8mip0 equus caball
44	496	57.7	174	2 Q6DHT8	Q6dht8 brachydanio
45	495	57.6	177	1 FRH3_XENLA	Q7sxa6 xenopus lae

ALIGNMENTS

RESULT 1
FRIL_HORSE ID FRIL_HORSE STANDARD; PRT; 174 AA.
AC P02791;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ferritin light chain (Ferritin L subunit).
GN Name=FTL;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93363645; PubMed=8357841; DOI=10.1016/0167-4781(93)90121-S;
RA Heusterspreute M., Crichton R.R.;
RT "Amino acid sequence of horse spleen apoferritin.";
RL FEBS Lett. 129:322-327(1981).
RN [3]
RP SEQUENCE.
RC TISSUE=Liver;
RA Mathijs J.M., Crichton R.R.;
RT "Amino acid sequence of horse liver ferritin.";
RL S. Afr. J. Sci. 80:424-426(1984).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=81052459; PubMed=7432529;
RA Clegg G.A., Stansfield R.F.D., Bourne P.E., Harrison P.M.;
RT "Helix packing and subunit conformation in horse spleen apoferritin.";
RL Nature 288:298-300(1980).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX PubMed=15299370;
RA Precigoux G., Yaviv J., Gallois B., Dautant A., Courseille C.,
RT "A crystallographic study of haem binding to ferritin.";
RL Acta Crystallogr. D 50:739-743(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=97303050; PubMed=9159481; DOI=10.1006/jmbi.1997.0970;
RA Hempstead P.D., Yewdall S.J., Fernie A.R., Lawson D.M., Artymluk P.J.,
RT Rice D.W., Ford G.C., Harrison P.M.;
"Comparison of the three-dimensional structures of recombinant human H
and horse L ferritins at high resolution.";

RL J. Mol. Biol. 268:424-448(1997).
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited.
CC -1- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
CC chain and H (heavy) chain. The major chain can be light or heavy,
CC depending on the species and tissue type.
CC -1- MISCELLANEOUS: In horse spleen the light chain is the major chain.
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D14523; BAA03396.1; -.
DR PIR; S36118; FRHOL.
DR PDB; 1AEW; X-ray; @=1-174.
DR PDB; 1DAT; X-ray; @=1-174.
DR PDB; 1GWG; X-ray; A=1-174.
DR PDB; 1HRS; X-ray; @=1-174.
DR PDB; 1IER; X-ray; @=1-174.
DR PDB; 1IES; X-ray; A/B/C/D/E/F=1-174.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN_LIKE; 1.
KW 3D-structure; Acetylation; Direct protein sequencing; Iron;
KW Iron storage; Metal-binding.
FT INIT MET 0
FT DOMAIN 6 155 Ferritin-like diiron.
FT DOMAIN 53 60 Catalytic site for iron oxidation.
FT MOD_RES 1 1 N-acetyls erine.
FT METAL 53 53 Iron (Potential).
FT METAL 56 56 Iron (Potential).
FT METAL 57 57 Iron (Potential).
FT METAL 60 60 Iron (Potential).
FT METAL 63 63 Iron (Potential).
FT CONFLICT 93 93 P -> L (in Ref. 2 and 3).
FT CONFLICT 135 137 DEE -> NEQ (in Ref. 3).
FT HELIX 10 36
FT TURN 37 38
FT TURN 40 42
FT HELIX 45 72
FT TURN 73 73
FT HELIX 92 120
FT TURN 121 121
FT HELIX 123 132
FT TURN 133 133
FT HELIX 134 157
FT HELIX 159 169
FT TURN 170 170
SQ SEQUENCE 174 AA; 19830 MW; AE039CA1BD046D4F CRC64;
Query Match 97.6%; Score 839; DB 1; Length 174;
Best Local Similarity 97.6%; Pred. No. 7.5e-62;
Matches 163; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YSTEVEAAVNRLVNLIRASVTVLSLGFYFDRDVALLEGVCHFFRELAEKREGAERLLK 60
Db 8 YSTEVEAAVNRLVNLIRASVTVTVLSLGFYFDRDVALLEGVCHFFRELAEKREGAERLLK 67

OY 61 MONORGRALFODLQPSODEWGTTPDAMKAIVLEKSLNQAALDLHALGSKADPHLCD 120
Db 68 MONORGRALFODLQPSODEWGTTPDAMKAIVLEKSLNQAALDLHALGSAQADPHLCD 127
OY 121 FLESHFLDEEVKLIKMGDHLTNIOQLVSKPGGLEYLFEKTLTKHD 167
Db 128 FLESHFLDEEVKLIKMGDHLTNIOQLVSKPGGLEYLFEKTLTKHD 174
RESULT 2
FRIL_HUMAN STANDARD; PRT; 174 AA.
ID P02792; Q9BTZ8;
AC 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ferritin light chain (Ferritin L subunit).
GN Name=FTL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86176772; PubMed=3754330;
RA Santoro C., Marone M., Ferrone M., Costanzo F., Colombo M.,
RA Minganti C., Cortese R., Silengo L.;
RT "Cloning of the gene coding for human L apoferritin.";
RL Nucleic Acids Res. 14:2863-2876(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85216457; PubMed=3858810;
RA Dörner M.H., Salfeld J., Will H., Leibold E.A., Vass J.K., Munro H.N.;
RT "Structure of human ferritin light subunit messenger RNA: comparison
RT with heavy subunit message and functional implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3139-3143(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86008223; PubMed=3840162;
RA Boyd D., Vecoli C., Belcher D.M., Jain S.K., Drysdale J.W.;
RT "Structural and functional relationships of human ferritin H and L
RT chains deduced from cDNA clones.";
RL J. Biol. Chem. 260:11755-11761(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Skin, and Urinary bladder;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boufard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 32-174 FROM N.A.
RX MEDLINE=87064341; PubMed=3023856;
RA Chou C.-C., Gatti R.A., Fuller M.L., Concannon P., Wong A., Chada S.,
RA Davis R.C., Salser W.A.;
RT "Structure and expression of ferritin genes in a human promyelocytic

RT cell line that differentiates in vitro.";
RL Mol. Cell. Biol. 6:566-573(1986).
RN (6)
RP SEQUENCE OF 1-35 AND 40-174.
RC TISSUE=Liver;
RX MEDLINE=84085077; Pubmed=6653779; DOI=10.1016/0014-5793(83)80037-4;
RA Addison J.M., Filton J.E., Lewis W.G., May K., Harrison P.M.;
RT "The amino acid sequence of human liver apoferritin.";
RL FEBS Lett. 164:139-144(1983).
RN (7)
RP SEQUENCE OF 83-89 AND 144-154.
RC TISSUE=Placenta;
RX Pubmed=8706699;
RA Vladimirov S.N., Ivanov A.V., Karpova G.G., Musolyamov A.K.,
RT Egorov T.A., Thiede B., Wittmann-Liebold B., Otto A.;
RT "Characterization of the human small-ribosomal-subunit proteins by N-
terminal and internal sequencing, and mass spectrometry.";
RL Eur. J. Biochem. 239:144-149(1996).
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited.
CC -1- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
CC chain and H (heavy) chain. The major chain can be light or heavy,
CC depending on the species and tissue type.
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M11147; AAA52439.1; -.
DR EMBL; M10119; AAA35831.1; -.
DR EMBL; M12938; AAA52440.1; -.
DR EMBL; BC002991; AAH02991.2; -.
DR EMBL; BC004245; AAH04245.1; -.
DR EMBL; BC008439; AAH08439.1; -.
DR EMBL; BC016346; AAH16346.1; -.
DR EMBL; BC016354; AAH16354.1; -.
DR EMBL; BC018990; AAH18990.1; -.
DR EMBL; BC058820; AAH58820.1; -.
DR EMBL; X03742; CAA27382.1; -.
DR EMBL; X03743; CAA27383.1; -.
DR EMBL; X03743; CAA27384.1; -.
DR PIR; B23920; FRHUL.
DR HSSP; P29391; 1LB3.
DR Genew; HGNC:3999; FTL.
DR H-INVD; HIX0015310; -.
DR MIM; 134790; -.
DR GO; GO:0008043; C:ferritin complex; TAS.
DR GO; GO:0005506; F:iron ion binding; TAS.
DR GO; GO:0006879; P:iron ion homeostasis; TAS.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN LIKE; 1.
KW Acetylation; Direct protein sequencing; Iron; Iron storage;
KW Metal-binding.
KW INIT MET 0
FT DOMAIN 6 155 Ferritin-like diiron.
FT DOMAIN 53 60 Catalytic site for iron oxidation.
FT MOD_RES 1 1 N-acetylsertine.

FT METAL 53 53 Iron (Potential).
FT METAL 56 56 Iron (Potential).
FT METAL 57 57 Iron (Potential).
FT METAL 60 60 Iron (Potential).
FT METAL 63 63 Iron (Potential).
FT CONFLICT 53 53 E -> Q (in Ref. 5).
FT CONFLICT 86 86 E -> Q (in Ref. 5).
FT CONFLICT 88 88 E -> W (in Ref. 7).
FT CONFLICT 101 101 A -> T (in Ref. 2).
FT CONFLICT 153 153 R -> A (in Ref. 7).
FT CONFLICT 174 174 D -> N (in Ref. 5).
SQ SEQUENCE 174 AA; 19888 MW; 8F0B4B23B6CAFEF2 CRC64;

Query Match 87.9%; Score 756; DB 1; Length 174;
Best Local Similarity 86.2%; Pred. No. 5.9e-55;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLNLYLRASYYTSLGFFYFDRDVALGVCHFFRELAEEKREGARLLK 60
Db 8 YSTDVEAAVNSLVNLYIQASTYTLSLGFYFDRDVALGVSHFFRELAEEKREGARLLK 67

QY 61 MONQGGRALFQDLQKPSQDEWGTTPDAMKAATVLEKSLNQALLDLHALGSKADPHLCD 120
Db 68 MONQGGRALFQDIKPAEDEMCKTPDAMKAAMALEKKNQALLDLHALGSAARTDPHLCD 127

QY 121 FLESHFLDEEVKLIRKGDHLTNIQRLVKSKAGLGEYLFERLTCLKHD 167
Db 128 FLETHFLDEEVKLIRKGDHLTNLHRLGPEAGLGEYLFERLTCLKHD 174

RESULT 3
Q7Z2W1 PRELIMINARY; PRT; 241 AA.
ID Q7Z2W1
AC Q7Z2W1; 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686L19147 (Fragment).
GN Name=DKFZp686L19147;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human colon endothel primary cell culture;
RG The German Human cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Well B., Amid C., Osanger A.,
RL Fobo G., Han M., Wiemann S.;
CC Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; BX571748; CAE11873.1; -.
DR HSSP; P02791; 1GMG.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN LIKE; 1.
KW Hypothetical protein; Iron; Iron storage; Metal-binding.


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FT  NON TER      1      1
SQ  SEQUENCE      241 AA;  26825 MW;  95D197E118824DE1 CRC64;

Query Match
Best Local Similarity  87.9%; Score 756; DB 2; length 241;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

OY  1 YSTEVEAAVNLVNLVLRASYTYLSLGFYFDRDDVALLEGVCHFFRELAEEKREGARLLK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  75 YSTDVEAAVNSLVNLVLRQASYTYLSLGFYFDRDDVALLEGVSHFFRELAEEKREGYERLLK 134

OY  61 MONQGRGGRALFQDLQKPSODEWGTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  135 MONQGRGGRALFQDIKKPADEWGKTPDAMKAAMALEKTLNQALLDLHALGSARTDPHLCD 194

OY  121 FLESHFLDEEVKLKKMGDHLTNIQRLVKSAGLGEYLFERLTLKHD 167
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  195 FLETHFLDEEVKLKKMGDHLTNLHRLGGPEAGLGEYLFERLTLKHD 241

RESULT 4
O6IBT7  PRELIMINARY; PRT; 175 AA.
AC  O6IBT7;
DT  05-JUL-2004 (TREMBlrel. 27, Created)
DT  05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  FTL protein.
GN  Name=FTL;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN  NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA  Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
    in a soluble, nontoxic, readily available form. The functional
    molecule, which is composed of 24 chains, is roughly spherical and
    contains a central cavity into which the polymeric ferric iron
    core is deposited (By similarity).
CC  -!- SIMILARITY: Belongs to the ferritin family.
CC  -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
EMBL; CR456715; CAG32996.1; -.
DR  HSSP; P02791; 1AEW.
DR  GO; GO:0005488; F:binding; IEA.
DR  GO; GO:0008199; F:ferric iron binding; IEA.
DR  GO; GO:0006879; P:iron ion homeostasis; IEA.
DR  GO; GO:0006826; P:iron ion transport; IEA.
DR  InterPro; IPR001519; Ferritin.
DR  InterPro; IPR009078; Ferritin/RR_like.
DR  InterPro; IPR008331; Ferritin Dps.
DR  InterPro; IPR009040; Ferritin_like.
DR  Pfam; PF00210; Ferritin; 1.
DR  ProDom; PD000971; Ferritin; 1.
DR  PROSITE; PS00540; FERRITIN_1; 1.
DR  PROSITE; PS00204; FERRITIN_2; 1.
DR  PROSITE; PS50905; FERRITIN LIKE; 1.
KW  Iron; Iron storage; Metal-binding.
SQ  SEQUENCE 175 AA; 19991 MW; C7726E91E1778D43 CRC64;

Query Match
Best Local Similarity  87.4%; Score 752; DB 2; length 175;
Matches 143; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

OY  1 YSTEVEAAVNLVNLVLRASYTYLSLGFYFDRDDVALLEGVCHFFRELAEEKREGARLLK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  9 YSTDVEAAANSLVNLVLRQASYTYLSLGFYFDRDDVALLEGVSHFFRELAEEKREGYERLLK 68

OY  61 MONQGRGGRALFQDLQKPSODEWGTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  69 MONQGRGGRALFQDIKKPADEWGKTPDAMKAAMALEKTLNQALLDLHALGSARTDPHLCD 128
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OY  121 FLESHFLDEEVKLKKMGDHLTNIQRLVKSAGLGEYLFERLTLKHD 167
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  129 FLETHFLDEEVKLKKMGDHLTNLHRLGGPEAGLGEYLFERLTLKHD 175

RESULT 5
O96AU9  PRELIMINARY; PRT; 175 AA.
ID  O96AU9
AC  O96AU9;
DT  01-DEC-2001 (TREMBlrel. 19, Created)
DT  01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT  01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Ferritin, light polypeptide.
GN  Name=FTL;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP  TISSUE=Kidney;
RC  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Uedl T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RT  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL  [2]
RN  SEQUENCE FROM N.A.
RP  TISSUE=Kidney;
RC  Strausberg R.;
RA  Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
    in a soluble, nontoxic, readily available form. The functional
    molecule, which is composed of 24 chains, is roughly spherical and
    contains a central cavity into which the polymeric ferric iron
    core is deposited (By similarity).
CC  -!- SIMILARITY: Belongs to the ferritin family.
CC  -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
EMBL; BC016715; AAH16715.1; -.
DR  HSSP; P29391; 1LB3.
DR  GO; GO:0005488; F:binding; IEA.
DR  GO; GO:0008199; F:ferric iron binding; IEA.
DR  GO; GO:0006879; P:iron ion homeostasis; IEA.
DR  GO; GO:0006826; P:iron ion transport; IEA.
DR  InterPro; IPR001519; Ferritin.
DR  InterPro; IPR009078; Ferritin/RR_like.
DR  InterPro; IPR008331; Ferritin Dps.
DR  InterPro; IPR009040; Ferritin_like.
DR  Pfam; PF00210; Ferritin; 1.
DR  ProDom; PD000971; Ferritin; 1.
DR  PROSITE; PS00540; FERRITIN_1; 1.
DR  PROSITE; PS00204; FERRITIN_2; 1.
DR  PROSITE; PS50905; FERRITIN LIKE; 1.
KW  Iron; Iron storage; Metal-binding.
SQ  SEQUENCE 175 AA; 19985 MW; 03B96E8F1F796B22 CRC64;
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Query Match      87.2%; Score 750; DB 2; Length 175;
Best Local Similarity 85.6%; Pred. No. 1.9e-54;
Matches 143; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY      1 YSTEVEAAVNRVLVNLVLRASYTYLSLGFYFDRDDVALGVCVHFFRELAEEKREGAERLLK 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      9 YSTDVEAAVNSLVNLVYLQASYTYLSLGFYFDRDDVALGVSHPFRELAEEKREGYERLLK 68

QY      61 MONORGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      69 MONORGRALLQDIKKPADEWGTTPDAMKAAMALEKKNQALLDLHALGSARTDPHLCD 128

QY      121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTCLKHD 167
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTCLKHD 175

RESULT 6
Q96CU0      PRELIMINARY; PRT; 175 AA.
AC      Q96CU0;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Ferritin, light polypeptide.
GN      Name=FTL;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buétow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Strausberg R.;
RL      Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC      in a soluble, nontoxic, readily available form. The functional
CC      molecule, which is composed of 24 chains, is roughly spherical and
CC      contains a central cavity into which the polymeric ferric iron
CC      core is deposited (By similarity).
CC      -1- SIMILARITY: Belongs to the ferritin family.
CC      -1- SIMILARITY: Contains 1 ferritin-like diron domain.
DR      EMBL; BC013928; AAH13928.1; -.
DR      HSSP; P29391; 1LB3.
DR      GO; GO:0005488; F:binding; IEA.
DR      GO; GO:0008199; F:ferric iron binding; IEA.
DR      GO; GO:0006879; P:iron ion homeostasis; IEA.
DR      GO; GO:0006826; P:iron ion transport; IEA.
DR      InterPro; IPR001519; Ferritin.

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DR      InterPro; IPR009078; Ferritin/RR_like.
DR      InterPro; IPR008331; Ferritin_Dps.
DR      InterPro; IPR009040; Ferritin_like.
DR      Pfam; PF00210; Ferritin; 1.
DR      ProDom; PD000971; Ferritin; 1.
DR      PROSITE; PS00540; FERRITIN_1; 1.
DR      PROSITE; PS00204; FERRITIN_2; 1.
DR      PROSITE; PS00905; FERRITIN LIKE; 1.
KW      Iron; Iron storage; Metal-binding.
SQ      SEQUENCE 175 AA; 20039 MW; 0DB9915724EB0BC2 CRC64;

Query Match      87.0%; Score 748; DB 2; Length 175;
Best Local Similarity 85.6%; Pred. No. 2.7e-54;
Matches 143; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY      1 YSTEVEAAVNRVLVNLVLRASYTYLSLGFYFDRDDVALGVCVHFFRELAEEKREGAERLLK 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      9 YSTDVEAAVNSLVNLVYLQASYTYLSLGFYFDRDDVALGVSHPFRELAEEKREGYERLLK 68

QY      61 MONORGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      69 MONORGRALLQDIKKPADEWGTTPDAMKAAMALEKKNQALLDLHALGSARTDPHLCD 128

QY      121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEYLFERLTCLKHD 167
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTCLKHD 175

RESULT 7
Q8WU07      PRELIMINARY; PRT; 175 AA.
AC      Q8WU07;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Ferritin, light polypeptide.
GN      Name=FTL;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buétow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      Strausberg R.;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC      in a soluble, nontoxic, readily available form. The functional
CC      molecule, which is composed of 24 chains, is roughly spherical and

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CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; BC021670; AAH21670.1; -.
DR HSSP; P29391; 1LB3.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 20062 MW; 18ADD1D0BA8C6A69 CRC64;

Query Match          86.9%; Score 747; DB 2; Length 175;
Best Local Similarity 85.6%; Pred. No. 3.3e-54;
Matches 143; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCHFFRELAEEKREGAERLLK 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 YSTDVEAAVNSLVNLVYLQASYYTSLGFYFDRDDVALGVSHFFRELAEEKREGYERLLK 68

QY 61 MONQGRGALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 MONQVRGALFQDIKKPAEDEWGKTPDAMKAAAMALEKKLNQALLDLHALGSARTDPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVSKSKAGLGEYLFERLTLTKHD 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLTKHD 175
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RESULT 8
Q86WT9 PRELIMINARY; PRT; 175 AA.
ID Q86WT9
AC Q86WT9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Ferritin-like protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li X., Obunike J., Tilson M.D.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; AY207005; AAO52739.1; -.
DR HSSP; P29391; 1LB3.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN_LIKE; 1.
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KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 19986 MW; 61596E6FF5932F82 CRC64;

Query Match          86.6%; Score 745; DB 2; Length 175;
Best Local Similarity 85.0%; Pred. No. 4.8e-54;
Matches 142; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCHFFRELAEEKREGAERLLK 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 YSTDVEAAVDSLNLVYLQASYYTSLGFYFDRDDVALGVSHLFFRELAEEKREGYERLLK 68

QY 61 MONQGRGALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 MONQGRGALFQDIKKPAEDEWGKTPDAMKAAAMALEKKLNQALLDLHALGSARTDPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVSKSKAGLGEYLFERLTLTKHD 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGPEAGLGEYLFERLTLTKHD 175
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RESULT 9
Q9JUM8 PRELIMINARY; PRT; 175 AA.
ID Q9JUM8
AC Q9JUM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Ferritin light chain.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20218664; PubMed=10753629; DOI=10.1006/bbrc.2000.2425;
RA Cheng Q., Gonzalez P., Zigler J.S. Jr.;
RT "High level of ferritin light chain mRNA in lens.";
RL Biochem. Biophys. Res. Commun. 270:349-355(2000).
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; AF233445; AAF36408.1; -.
DR PIR; JC7238; JC7238.
DR HSSP; P02791; 1GWG.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 19944 MW; 2BC53200ADE4E109 CRC64;

Query Match          86.6%; Score 745; DB 2; Length 175;
Best Local Similarity 85.6%; Pred. No. 4.8e-54;
Matches 143; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCHFFRELAEEKREGAERLLK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 YSTEVEAAVNRLVNLVYLQASYYTSLGFYFDRDDVALAGVGHFFRELAEEKREGAERLLK 68

QY 61 MONQGRGALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
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FT METAL 63 63 Iron (Potential).
SQ SEQUENCE 174 AA; 19943 MW; B9B03050B233BB86 CRC64;

Query Match
Best Local Similarity 85.8%; Score 738; DB 1; Length 174;
Matches 143; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCCHFFRELAEEKREGAERLLK 60
Db 8 YSPEVEAAVNHLVNLHLRASVYTYLSLGFYFDRDDVALGVSCHFFRELAEEKREGAERLLK 67

QY 61 MONORGGRALFQDLQKPSODEWGTTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
Db 68 MONORGGRALFQDVQKPSODEWGKTLNAMEAALALEKNLNLQALLDLHALGSAHTDPHLCD 127

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGELYLFERLTLKHD 167
Db 128 FLENHFLDEEVKLIKMGDHLTNIRRLSGPQASLGELYLFERLTLKHD 174

RESULT 12
Q9BYW6 PRELIMINARY; PRT; 175 AA.
ID Q9BYW6
AC Q9BYW6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE DJ68IN20.2 (Novel protein similar to ferritin, light polypeptide
DE (FTL)).
GN Name=dj68IN20.2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; AI031670; CAB43181.1; -.
DR HSSP; P29391; 1LB3.
DR Genew; HGNC:4000; FTLL1.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 20075 MW; ECCCB80AF109F8BD CRC64;

Query Match
Best Local Similarity 85.0%; Score 731; DB 2; Length 175;
Matches 140; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCCHFFRELAEEKREGAERLLK 60
Db 9 YSTDVEAAVNSLVNLVQLASVYTYLSLGFYFDRDDALGVSCHFFRELTEEKREGYERLLK 68

QY 61 MONORGGRALFQDLQKPSODEWGTTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
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Db 69 MONORGGRALFQDIKKPADEWGKTPDAMKAAAMALEKKNQALLDLHALDSAHMDPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGELYLFERLTLKH 166
Db 129 FLETHFLDEEVKLIKMGDHLTNLHRLGCPAAGLGELYLFERLTLKH 174

RESULT 13
Q9JKP6 PRELIMINARY; PRT; 175 AA.
ID Q9JKP6
AC Q9JKP6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Ferritin light chain.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Sevoz C., Buronfosse T.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; AF230928; AAF68948.1; -.
DR HSSP; P02791; 1GMG.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 19904 MW; 85FDDCD31546696A CRC64;

Query Match
Best Local Similarity 85.0%; Score 731; DB 2; Length 175;
Matches 141; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDDVALGVCCHFFRELAEEKREGAERLLK 60
Db 9 YSTEVEAAVNRLVNLHLQASYTYLSLGFYFDRDDVALAGVGHFFRELAEEKREGAERLLK 68

QY 61 MONORGGRALFQDLQKPSODEWGTTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
Db 69 TONORGGRALFQDVQKPSODEWGKTLNAMEAALTLEKSLNQALLDLHALGSAKTDSHVCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGELYLFERLTLKHD 167
Db 129 FLENHFLDEEVKLIKIGDHLTNLRLDGPQAGLGELYLFERLTLKHD 175

RESULT 14
Q6P7T1 PRELIMINARY; PRT; 183 AA.
ID Q6P7T1
AC Q6P7T1;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
```



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DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diron domain.
DR EMBL: BC061525; AAH61525.1; -.
DR HSSP: P02791; 1AEW.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001519; Ferritin.
DR InterPro: IPR009078; Ferritin/RR like.
DR InterPro: IPR008331; Ferritin_Dps.
DR InterPro: IPR009040; Ferritin_like.
DR Pfam: PF00210; Ferritin; 1.
DR ProDom: PD000971; Ferritin; 1.
DR PROSITE: PS00540; FERRITIN_1; 1.
DR PROSITE: PS00204; FERRITIN_2; 1.
DR PROSITE: PS50905; FERRITIN LIKE; 1.
DR Hypothetical protein; Iron; Iron storage; Metal-binding.
SQ SEQUENCE 183 AA; 20748 MW; E6AB306251D55106 CRC64;

Query Match 84.7%; Score 728; DB 2; Length 183;
Best Local Similarity 80.6%; Pred. No. 1.3e-52;
Matches 141; Conservative 17; Mismatches 9; Indels 8; Gaps 1.

OY 1 YSTEVEAAVNRLVNLTYLRASYTYTISLGFFPDRDDVALGVCCHFFRELAEEKREGAERLLK 60
DB 9 YSTEVEAAVNRLVNLHLRASITYTISLGFFPDRDDVALGVCCHFFRELAEEKREGAERLLK 68
OY 61 MONQRCGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 69 LQNERGGRALFQDVQKPSQDEWGTTEAMEAALALEKLNQALLDLHALGSARTDPHLCD 128
OY 121 FLESHPLDEBVKLIKMGDHLTNIQRLV-----KSKAGLGEYLFERLLTLKGD 167

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Db          129 FLESHFLDKEVKLIKMGNHLTNLRRVAGPQPAQTGVAQASLGYYLPERLTKHD 183

RESULT 15
FRIL_RAT
ID FRIL_RAT STANDARD; PRT; 182 AA.
AC P02753;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ferritin light chain (Ferritin L subunit).
GN Name=Fcl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=87222340; PubMed=3584116;
RA Leibold E.A., Munro H.N.;
RT "Characterization and evolution of the expressed rat ferritin light
RT subunit gene and its pseudogene family. Conservation of sequences
RT within noncoding regions of ferritin genes.";
RL J. Biol. Chem. 262:7335-7341(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=84162134; PubMed=6546756;
RA Leibold E.A., Aziz N., Brown A.J.P., Munro H.N.;
RT "Conservation in rat liver of light and heavy subunit sequences of
RT mammalian ferritin. Presence of unique octopeptide in the light
RT subunit.";
RL J. Biol. Chem. 259:4327-4334(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210224; PubMed=1555892;
RA Denis M.G.;
RT "Isolation of cDNA clones corresponding to genes differentially
RT expressed in two colon-carcinoma cell lines differing by their
RT tumorigenicity.";
RL Int. J. Cancer 50:930-936(1992).
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited.
CC -1- TISSUE SPECIFICITY: In rat liver, the light chain is the major
CC chain.
CC -1- DOMAIN: The rat light chain has an octopeptide insertion after
CC residue 158 compared with other light chains.
CC -1- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
CC chain and H (heavy) chain. The major chain can be light or heavy,
CC depending on the species and tissue type.
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K01930; AAA41154.1; -.
CC EMBL; J02741; AAA41155.1; -.
CC EMBL; L01122; AAA41152.1; -.
CC PIR; A29575; FRRTL.
CC PIR; I54774; I54774.
CC HSSP; P29391; 1LB3.
CC InterPro; IPR001519; Ferritin.
CC InterPro; IPR009078; Ferritin/RR like.

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DR InterPro; IPR008331; Ferritin Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS50905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
FT INIT MET 0
FT DOMAIN 6 155 Ferritin-like diiron.
FT METAL 53 53 Iron (Potential).
FT METAL 56 56 Iron (Potential).
FT METAL 57 57 Iron (Potential).
FT METAL 60 60 Iron (Potential).
FT METAL 63 63 Iron (Potential).
FT CONFLICT 97 97 E -> K (in Ref. 2).
FT CONFLICT 120 121 RT -> QA (in Ref. 2).
FT CONFLICT 125 125 L -> F (in Ref. 3).
FT CONFLICT 154 154 V -> W (in Ref. 2).
FT CONFLICT 155 155 Q -> A (in Ref. 3).
SQ SEQUENCE 182 AA; 20674 MW; 3D3DEBCE5088655B CRC64;

Query Match 84.4%; Score 726; DB 1; Length 182;
Best Local Similarity 80.6%; Pred. No. 1.9e-52;
Matches 141; Conservative 17; Mismatches 9; Indels 8; Gaps 1;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSIGFYFDRDDVALGVCHFFRELAEEKREGAERLLK 60
Db 8 YSTEVEAAVNRLVNLVLRASYTYLSIGFFPDRDDVALEGVGHFFRELAEEKREGAERLLK 67
QY 61 MONQRCGRALFQDLQKPSQDEWGTTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
Db 68 LQNERGGRALFQDVQKPSQDEWGKTLEAMEALALEKNINQALLDLHALGSARTDPHLCD 127
QY 121 FLESHFLDEEVKLKKMGDHLTNIQRLV-----KSKAGLGEYLFERLTCLKHD 167
Db 128 FLESHFLDKEVKLIKKGNNHLTNLRVQGPQPAQTGVAQASLGEYLFERLTCLKHD 182

Search completed: August 22, 2005, 09:10:08
Job time : 174 secs